

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: January 31, 2004, 01:41:46 ; Search time 15.5 Seconds

(without alignments)
3324.815 Million cell updates/sec

Title: US-10-021-323-13

Perfect score: 1100

Sequence: 1 ggaatgaacaaactttt.....tgaagcttacaactaag 609

Scoring table:

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Xgapop 10.0 , Xgapext 0.5	
Fgapop 10.0 , Fgapext 0.5	
Delop 6.0 , Delext 7.0	

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 657434

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=Issued_Patents_AA -QEXT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0
-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blousum62 -TRANS=human40.cdt
-LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOC
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- Issued_Patents_AA:*
- 1: /cg2_6/ptodata/2/1aa/5A_COMB.pep:*
 - 2: /cg2_6/ptodata/2/1aa/5B_COMB.pep:*
 - 3: /cg2_6/ptodata/2/1aa/6A_COMB.pep:*
 - 4: /cg2_6/ptodata/2/1aa/6B_COMB.pep:*
 - 5: /cg2_6/ptodata/2/1aa/6CTUS_COMB.pep:*
 - 6: /cg2_6/ptodata/2/1aa/backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	159	15.0	149	3	US-08-963-409-3
2	155	14.6	150	2	US-09-239-909-2
3	152.5	14.4	160	2	US-08-602-941-1
4	152.5	14.4	160	4	US-08-961-264-1
5	152.5	14.4	160	4	US-09-442-099A-1
6	152.5	14.4	160	4	US-09-612-342-1
7	147	13.9	150	3	US-09-239-909-4
8	147	13.9	147	2	US-08-818-252-2
9	147	13.9	642	2	US-08-818-252-2
10	147	13.9	652	2	US-08-818-253-4
11	147	13.9	652	3	US-08-818-252-4
12	145.5	13.7	456	1	US-08-464-164-2

13	145.5	13.7	456	1	US-08-338-057-2	Sequence 2, Appli
14	145.5	13.7	456	2	US-08-668-416-2	Sequence 2, Appli
15	145	13.7	149	1	US-08-100-874-2	Sequence 2, Appli
16	144.5	13.6	152	3	US-08-963-409-5	Sequence 5, Appli
17	144	13.6	642	2	US-08-818-253-6	Sequence 6, Appli
18	144	13.6	642	2	US-08-818-252-6	Sequence 8, Appli
19	144	13.6	656	2	US-08-818-253-8	Sequence 8, Appli
20	144	13.6	656	2	US-08-818-252-8	Sequence 8, Appli
21	143	13.5	408	1	US-07-951-715A-21	Sequence 21, Appli
22	143	13.5	408	2	US-08-459-448A-21	Sequence 21, Appli
23	143	13.5	408	3	US-08-459-555A-21	Sequence 21, Appli
24	143	13.5	408	3	US-08-459-504B-21	Sequence 21, Appli
25	143	13.5	408	3	US-08-459-444-21	Sequence 21, Appli
26	143	13.5	408	4	US-09-547-442-21	Sequence 22, Appli
27	143	13.5	464	1	US-07-951-715A-22	Sequence 22, Appli
28	143	13.5	464	2	US-08-459-448A-22	Sequence 22, Appli
29	143	13.5	464	3	US-08-459-555A-22	Sequence 22, Appli
30	143	13.5	464	3	US-08-459-504B-22	Sequence 22, Appli
31	143	13.5	464	3	US-08-459-444-22	Sequence 0, Appli
32	143	13.5	464	4	US-09-547-442-22	Sequence 0, Appli
33	141	13.3	149	3	US-08-963-409-4	Sequence 4, Appli
34	141	13.3	149	3	US-08-641-873-20	Sequence 20, Appli
35	133	12.3	145	3	US-08-720-625-5	Sequence 5, Appli
36	132	12.4	142	1	US-07-951-715A-24	Sequence 24, Appli
37	132	12.4	142	2	US-08-459-448A-24	Sequence 24, Appli
38	132	12.4	142	3	US-08-459-555A-24	Sequence 24, Appli
39	132	12.4	142	3	US-08-459-504B-24	Sequence 24, Appli
40	132	12.4	142	3	US-08-459-444-24	Sequence 24, Appli
41	132	12.4	142	4	US-09-547-442-24	Sequence 24, Appli
42	127.5	12.0	146	4	US-08-963-409-1	Sequence 1, Appli
43	121.5	11.5	179	3	US-08-764-563-4	Sequence 4, Appli
44	120.5	11.4	247	4	US-09-368-819A-2	Sequence 2, Appli
45	120.5	11.4	264	4	US-09-368-819A-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-963-409-3
; Sequence 3, Application US/08963409
; Patent No. 6046315
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: DISEASE ASSOCIATED CALMODULIN PROTEIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/963,409
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: pf-0418 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 149 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 385234
US-08-963-409-3

Alignment Scores:
Pred. No.: 5,12e-10 Length: 149
Score: 159.00 Matches: 44
Percent Similarity: 50.00% Conservative: 39
Best Local Similarity: 26.51% Mismatches: 55
Query Match: 14.99% Indels: 28
DB: Gaps: 6

US-10-021-323-13 (1-609) x US-08-963-409-3 (1-149)

QY 550 AAAATGTCCTCCCTTAGTAAGACCGACTTGCAACGGTATTGAGAGCTGCAGAGAAAT 491
DB 4 LysleuThrGluGluGlnIleSerGluPheLysGluAlaPheSerLeuPheAsp 23
QY 490 GGAGATGGCTTCTAGTCTGAGAGAGCTGAATTGCTGCTCAGAGATCCGG----- 437
DB 24 GlyAspGlyThrIleThrIleThrIleGluLeuGlyThrIleValMetArgSerLeuGlnIle 43
QY 436 -----TCTGTCCAATTCAACCTTGAAAGATTGGAGCCCTTGAAGTGAAGAACCA 389
DB 44 ProThrGluAlaGluLeuGlnIleAspMetIleAsnGluIleAsp---ThrAspGlyAsnGly 62
QY 388 TGTTCGACCTTGATGATATCTTGTCTTTATGATCATCATGCAACCCACTGCGACAT 329
DB 63 ThrIleAspPheProGluPheLeuThrIle-----MetAlaArgLysLeuLys--- 78
QY 328 GGTGTGTCAGAGAGAGAGAGAGAGATGTGTCATTCAACGGCGCGGTGAAGAGAGAGAC 269
DB 79 -----AspThrAspThrGluGluGluLeuIle----- 87
QY 268 AGTGCCTTGGCAGAGCTTTTAAAGTCTTGAAGTGGATGGGATGGGAGATGT 209
DB 88 -----GluAlaPheArgValPheAspArgAspGlyAspGlyTyrIleSerAla 103
QY 208 GAGGAGCTTGATGATGCTGCTGCGAAGACCTGGTATGTCAGGAAATAGTGAAAGAC 149
DB 104 AspGluLeuArgHisValMetThrAsnLeuGly-----GluLysLeuThrAsnGluGlu 121
QY 148 TGCAGAGCATGATTTGGTATTACGACACCAATTCAGACGGCATGTTGATTTTCAGAA 89
DB 122 ValAspGluMetIleArgGluAlaAspIleAspGlyAspGlyGlnIleAsnTyrGluGlu 141
QY 88 TTCAAAAACATCATGTGA 71
DB 142 PheValLysMetMetIle 147

RESULT 2

US-09-239-909-2
Sequence 2, Application US/09239909
Patent No. 6284952
GENERAL INFORMATION:
APPLICANT: Kumbo Petrochemical Co. Ltd.
TITLE OF INVENTION: Transgenic Plants with Divergent SCAM4 or SCAM5 Gene to Achieve N
FILE REFERENCE: P99-2-6
CURRENT APPLICATION NUMBER: US/09/239,909
EARLIER FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: EP 99300136.1
NUMBER OF SEQ ID NOS: 4
SOFTWARE: KODATIN 1.0
SEQ ID NO 2
LENGTH: 150
TYPE: PRT

ORGANISM: G. max calmodulin4 (SCAM4)
US-09-239-909-2

Alignment Scores:
Pred. No.: 1.5e-09 Length: 150
Score: 155.00 Matches: 47
Percent Similarity: 47.20% Conservative: 29
Best Local Similarity: 29.19% Mismatches: 57
Query Match: 14.61% Indels: 28
DB: Gaps: 5

US-10-021-323-13 (1-609) x US-09-239-909-2 (1-150)

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DB 12 AspPheLysGluAlaPheGlyLeuPheAspLysAspGlyAspGlyCysIleThrValGlu 31
QY 466 GAGCTGAATTGGTCTTCACAGAAATCGGCTGTCTCAATTCACTGAGCTTGAAGAAATGAG 407
DB 32 GluLeuAlaThrValIleArgSerLeuAspGln---AsnProThrGluGluGluLeuGln 50
QY 406 CCCTTAGG-----GAAACCATGTTGAAGCTTGATGATTTCTTG 365
DB 51 AspMetIleSerGluValAlaAspAlaAspGlyAsnGlyThrIleGluPheAspGluPheLeu 70
QY 364 TTTCTTTATGATTCATCTCGAACCCACTGCACATGCTGGTGACGAAGAGAGAGAG 305
DB 71 -----SerLeuMetAlaLysValLysValLysAspThrAspAlaGluGluGlu--- 85
QY 304 GAATGTGTCATTCAACGGCGGTGAAGAGAGACAGTGCCTTGCGAAGCTTTTAA 245
DB 86 -----LeuLysGluAlaPheLys 91
QY 244 GTGTTGACCTTGATGAGGATGCTGGGATGATGAGAGCTTGAATAGTCTGGA 185
DB 92 ValPheAspLysAspGlnAsnGlyTyrIleSerAlaSerGluLeuArgHisValMetIle 111
QY 184 AGACTGGTATGATGAGTGAATAATGCAAAAAGCTGCAGACAGCATGATTTGTAATTAC 125
DB 112 AsnLeuGly-----GluLysLeuThrAspGluIleValGluGlnMetIleLysGluAla 129
QY 124 GACACCAATTCAGACGGCATGTTGATTTTCAGAAATTCAAAACATGATTTACATTC 65
DB 130 AspLeuAspGlyAspGlyGlnValAsnTyrGluGluPheValLysMetMetThrVal 149
QY 64 CGT 62
DB 150 Arg 150

RESULT 3

US-08-602-941-1
Sequence 1, Application US/08602941
Patent No. 5837680
GENERAL INFORMATION:
APPLICANT: Moses, Marsha A.
APPLICANT: Langer, Robert S.
APPLICANT: Wiedersheim, Dimitri G.
APPLICANT: Wu, Immln
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: COMPRISING TROPONIN SUBUNITS, FRAGMENTS AND ANALOGS
TITLE OF INVENTION: THERMOF AND METHODS OF THEIR USE TO INHIBIT ANGIOGENESIS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

```

1 OPERATING SYSTEM: DOS
2 SOFTWARE: FastSEO Version 2.0
3 CURRENT APPLICATION DATA:
4 APPLICATION NUMBER: US/08/602,941
5 FILING DATE: 16-FEB-1996
6 CLASSIFICATION: 514
7 ATTORNEY/AGENT INFORMATION:
8 NAME: Polissant, Brian M.
9 REGISTRATION NUMBER: 28,452
10 REFERENCE/DOCKET NUMBER: 8657-021-999
11 TELECOMMUNICATION INFORMATION:
12 TELEPHONE: 212-790-9090
13 TELEFAX: 212-869-8864/9741
14 INFORMATION FOR SEQ ID NO: 1:
15 SEQUENCE CHARACTERISTICS:
16 LENGTH: 160 amino acids
17 TYPE: amino acid
18 STRANDEDNESS: single
19 TOPOLOGY: linear
20 MOLECULE TYPE: No. 5837680e
21 FEATURE:
22 NAME/KEY: Peptide
23 LOCATION: 1..160
24 OTHER INFORMATION:
25 OTHER INFORMATION: Muscle troponin C

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Alignment Scores:	
Pred. No.:	3e-09
Score:	157.50
Percent Similarity:	45.86%
Best Local Similarity:	27.39%
Query Match:	14.37%
DB:	2
Gaps:	4
Length:	160
Matches:	43
Conservative:	29
Mismatches:	60
Indels:	25
Gaps:	4

US-10-021-323-13 (1-609) x US-08-602-941-1 (1-160)

Oy	526	GACTTGCAACGCGCTATTCCAGAAAGCTTCACAAGAATGGAGATGCCTTGTGAATGCTGAG	46
Db	19	GlunpheylsAlaIlaheaspwctephedapalaaspglyglYlaasplIssevallys	38
Oy	466	GAGCTGAATGTGTTGCCAGAGAAATCGGSGTCGTTCCAATTACAGCCTTGAAGAAATGGAG	407
Db	39	GIUncluglThryValmetargetleuglyIntnrPro---ThrlYsglUdeulaasp	57
OY	406	CCCTTAGTG-----GAAAAACCATGTTTGACATTGGAATGAATTCCTG	365
Db	58	AlalIellegluInuValaepgluaesglysergylThrIlaeApheglugluNheleu	77
OY	364	TTCCTTTAATGAATTCATCTTCGAAACCACCTGGCACATGCTGCTGAGAGAGAGAGAGAG	307
Db	78	ValmetweValargImetelysgluAupaIalVsglyVsaserglugluIn-----	95
OY	304	GAATTGGTCATTCACGCGCGCGGTGAAGAAAGACATGACCTTGCAGAAAGCTTTTAAA	245
Db	96	-----LeuIIeglucyshearg	103
OY	244	GTCGTTGACTTGAATGCGGANTGGCTGTTGGGGGAGATGTGAAGACTTGAATTAAGTCTGGGA	185
Db	102	IleheaspArgasnIlaaspglyTryleaspProgIugluLeualaaglulIahearg	123
OY	184	AGACTGGGATGTGAGGCGTGAATAATAGCAAAGAACCTGCACAGACATATTTGGATTAAC	122
Db	122	Alaseerily-----GlunIseValIthrnaprglugluIlcgluseIseIumetelysaapoly	133
OY	124	GACACCAATTCAAGCGGATGTTGATTTTCAAGAATTCAAAAACATGATG	74
Db	140	AspyIasnaasnaspIyargrileaspPheaspGluNheuleulyamewet	156

RESULT 4
US-08-961-264-1
; Sequence 1, Application US/08961264
; Patent No. 6025331

GENERAL INFORMATION:
APPLICANT: Moses, Marsha A.
APPLICANT: Langer, Robert S.
APPLICANT: Wiederschain, Dimitri G.
APPLICANT: Wu, Immin
APPLICANT: Sytkowski, Arthur
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: COMBINING TROPONIN SUBUNITS
TITLE OF INVENTION: THEROF AND METHODS OF THEIR USE TO INHIBIT ANGIOGENESIS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,264
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,941
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Polissant, Brian M.
REGISTRATION NUMBER: 28,452
REFERENCE/DOCKET NUMBER: 8657-021-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 160 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6025331e
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..160
OTHER INFORMATION: /label= Human Fast Twitch Skeletal
OTHER INFORMATION: Muscle Troponin C

Pred. No.:	3e-09	Length:	16
Score:	152.50	Matches:	43
Percent Similarity:	45.86%	Conservative:	29
Best Local Similarity:	27.39%	Mismatches:	60
Query Match:	14.37%	Indels:	25
DB:	3	Gaps:	4

US-10-021-323-13 (1-609) X US-08-961-264-1 (1-160)

Oy	526	GAC	TTC	GCA	CGC	GTA	TTC	GAG	AAG	CTG	CGA	CA	AG	TGA	AG	TGC	CTT	CGT	TAG	CTG	GAG	467	
Db	19	Gln	Phe	Leu	Ala	Ala	Phe	Asp	Met	Phe	Asp	Ala	Asp	Gly	Gly	Val	Asp	Leu	Leu	Val	Leu	38	
Oy	466	GAC	TGA	ATT	GGT	GTC	CTC	CAG	AAG	ATC	GCG	ATC	CTG	CC	AAT	CAC	CTT	GTA	GAA	ATT	GAG	407	
Db	39	Gln	Leu	Gly	Thr	Val	Met	Arg	Met	Leu	Leu	Gly	Aln	His	Pro	---	Thr	Val	Gln	Leu	Leu	Asp	57
Oy	406	CC	CTT	AGT	G	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
Db	58	Ala	Leu	Gln	Glu	Val	Ala	Asp	Glu	Asp	Gly	Ser	Gly	Thr	Thr	Leu	Asp	Phe	Gln	Glu	Glu	77	
Oy	364	TTC	TTT	TAA	TAA	TCC	ATC	TCG	ACA	CCCA	CTG	GCA	CTG	GAT	GAT	GAT	GCA	GAA	GAG	GAG	GAG	305	

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DB 78 ValmetMetValArgGlnMetLysGluAspAlaIleValLysSerGlnGluGlu----- 95
QY 304 GAATTGTCATTACACGGCGCGGTGAAGAAGACAGTACCTTGCGAAGCTTTTAA 245
DB 96 -----LeuAlaGlnCysPheArg 101
QY 244 GTGTTTGACTGTAATGGGATGGGTTGGGGATGTGAGAGCTTGAATACCTGCTGGA 185
DB 102 IlePheAspArgAsnAlaAspGlyTyrIleAspProGlnGluLeuAlaGluIlePheArg 121
QY 184 AGACTGGGTATGTAGAGTGAAATAGTGAATAAGACTGCAGACATGATTTGGTATTAC 125
DB 122 AlaSerGly-----GluHisValThrAspGlnGluIleGluSerLeuMetLysAspGly 139
QY 124 GACACCAATTCAAGCGCATGTGATTTCAGAAATTCAAAACATGATG 74
DB 140 AspLysAsnAsnAspGlyArgIleAspPheAspGlnPheLeuLysMetMet 156

RESULT 5
US-09-442-099A-1
; Sequence 1, Application US/09442099A
; Patent No. 6465431
; GENERAL INFORMATION:
; APPLICANT: Thorn, R.
; APPLICANT: Lanser, M.
; APPLICANT: Moses, M.
; APPLICANT: Wiederschain, D.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING TROPONIN SUBUNITS,
; TITLE OF INVENTION: FRAGMENTS AND HOMOLOGS THEREOF AND METHODS OF THEIR USE, TO
; FILE REFERENCE: 8657-028
; CURRENT APPLICATION NUMBER: US/09/442,099A
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: 09/268,274
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: 08/961,264
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: 08/602,941
; PRIOR FILING DATE: 1996-02-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 160
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-442-099A-1

Alignment Scores:
Pred. No.: 3e-09 Length: 160
Score: 152.50 Matches: 43
Percent Similarity: 45.86% Conservative: 29
Best Local Similarity: 27.39% Mismatches: 60
Query Match: 14.37% Indels: 25
DB: 4 Gaps: 4

US-10-021-323-13 (1-609) x US-09-442-099A-1 (1-160)
QY 526 GACTTGCAACCGGATTCGAGAGCTCGACAAAGATGAGATGCTTGTAGTCTGAG 467
DB 19 GlnPheLysAlaAlaPheAspMetPheAspAlaAspGlyGlyAspIleSerValLys 38
QY 466 GAGCTGAATGCTGCTCCAGAGATCGGCTGTCTGCCATTACAGCTTGAAGAAATTTGAG 407
DB 39 GlnLeuGlyThrValMetArgMetLeuGlyGlnThrPro---ThrLysGlnGluLeuAsp 57
QY 406 CCTTATG-----GGAATAACATGTTGAACCTTGGAATTTCTTG 365
DB 58 AlaIleIleGlnGluValAspGluAspGlySerGlyThrIleAspPheGlnGluPheLeu 77
QY 364 TTCCTTTATGAATCATCTCGAACCCACTGCGACATGTGTGTGAGAAAGAGAGAGAG 305
DB 78 ValMetMetValArgGlnMetLysGluAspAlaIleValLysSerGlnGluGlu----- 95
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QY 304 GAATTGTCATTACACGGCGCGGTGAAGAAGACAGTACCTTGCGAAGCTTTTAA 245
DB 96 -----LeuAlaGlnCysPheArg 101
QY 244 GTGTTTGACTGTAATGGGATGGGTTGGGGATGTGAGAGCTTGAATACCTGCTGGA 185
DB 102 IlePheAspArgAsnAlaAspGlyTyrIleAspProGlnGluLeuAlaGluIlePheArg 121
QY 184 AGACTGGGTATGTAGAGTGAAATAGTGAATAAGACTGCAGACATGATTTGGTATTAC 125
DB 122 AlaSerGly-----GluHisValThrAspGlnGluIleGluSerLeuMetLysAspGly 139
QY 124 GACACCAATTCAAGCGCATGTGATTTCAGAAATTCAAAACATGATG 74
DB 140 AspLysAsnAsnAspGlyArgIleAspPheAspGlnPheLeuLysMetMet 156

RESULT 6
US-09-612-342-1
; Sequence 1, Application US/09612342
; Patent No. 6586401
; GENERAL INFORMATION:
; APPLICANT: Thorn, R.
; APPLICANT: Lanser, M.
; APPLICANT: Moses, M.
; APPLICANT: Wiederschain, D.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING
; TITLE OF INVENTION: TROPONIN SUBUNITS, FRAGMENTS AND HOMOLOGS THEREOF AND
; FILE REFERENCE: 8657-026
; CURRENT APPLICATION NUMBER: US/09/612,342
; PRIOR FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: US/09/268,274
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: 08/961,264
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: 08/602,941
; PRIOR FILING DATE: 1996-02-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 160
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-612-342-1

Alignment Scores:
Pred. No.: 3e-09 Length: 160
Score: 152.50 Matches: 43
Percent Similarity: 45.86% Conservative: 29
Best Local Similarity: 27.39% Mismatches: 60
Query Match: 14.37% Indels: 25
DB: 4 Gaps: 4

US-10-021-323-13 (1-609) x US-09-612-342-1 (1-160)
QY 526 GACTTGCAACCGGATTCGAGAGCTCGACAAAGATGAGATGCTTGTAGTCTGAG 467
DB 19 GlnPheLysAlaAlaPheAspMetPheAspAlaAspGlyGlyAspIleSerValLys 38
QY 466 GAGCTGAATGCTGCTCCAGAGATCGGCTGTCTGCCATTACAGCTTGAAGAAATTTGAG 407
DB 39 GlnLeuGlyThrValMetArgMetLeuGlyGlnThrPro---ThrLysGlnGluLeuAsp 57
QY 406 CCTTATG-----GGAATAACATGTTGAACCTTGGAATTTCTTG 365
DB 58 AlaIleIleGlnGluValAspGluAspGlySerGlyThrIleAspPheGlnGluPheLeu 77
QY 364 TTCCTTTATGAATCATCTCGAACCCACTGCGACATGTGTGTGAGAAAGAGAGAGAG 305
DB 78 ValMetMetValArgGlnMetLysGluAspAlaIleValLysSerGlnGluGlu----- 95
QY 304 GAATTGTCATTACACGGCGCGGTGAAGAAGACAGTACCTTGCGAAGCTTTTAA 245
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Db          96          -----Leu1aGlucYbhearg 101
Oy          244 GTGTTGACTTGATGGGATGGGTTGGGGGAGATGTGAGAGCTTGAATTACGTCGTGGGA 185
Db          102 lIepheapArgAsnAlaAspGlyYrIleAspProGluGluLeuAlaGluIlePhearg 121
Oy          184 AGACTGGGTATGTGAGGTGAATAATAGTGAAGAAAGACTGCAGAGGACATGATTGGATTAC 125
Db          122 AlaSerGly-----GluHisValThrAspGluGluIleGluSerLeuMetLeuAspGly 139
Oy          124 GACACCAATTGACAGCGCATGTTGATTCTTCAAGATTCAAAAATCATGATG 74
Db          140 AspLysAsnAsnAlaAspGlyArgIleAspPheAspGluPheLeuLysMetMet 156

RESULT 7
US-09-239-909-4
; Sequence 4, Application US/09239909
; Patent No. 6284952
; GENERAL INFORMATION:
; APPLICANT: Kumo Petrochemical Co. Ltd.
; TITLE OF INVENTION: Transgenic Plants with Divergent SCAM4 or SCAM5 Gene to Achieve N
; FILE REFERENCE: P99-2-6
; CURRENT APPLICATION NUMBER: US/09/239,909
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: EP 99300136.1
; EARLIER FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 4.
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 4
; LENGTH: 150
; TYPE: PRT
; ORGANISM: G. max calmodulins (SCAM5)
US-09-239-909-4

Alignment Scores:
Score: 1.27e-08 Length: 150
Percent Similarity: 147.00 Matches: 46
Best Local Similarity: 49.38% Conservative: 33
Query Match: 28.75% Mismatches: 51
DB: 13.85% Indels: 30
Gaps: 6

US-10-021-323-13 (1-609) x US-09-239-909-4 (1-150)

Oy          529 ACCGACTTGCAACGGCGATTTCGAGAGCTCGACAGAAGATGAGATGGCTTCTTAAGTCG 470
Db          11 SerGluIleLysGluAlaPheGlyLeuPheAspLysAspGlyAspGlyCysIleThrVal 30
Oy          469 GAGAGCTGGAATTTGGTCTCTCAGAGGATCGGCTGTGCCAATTC--AGCTTGAAGAA 413
Db          31 AspGluPheValThrValIleArgSerLeu-----ValGlnAsnProThrGluGluGlu 48
Oy          412 TTGAGCCCTTAGTG-----GGAAAACCATGTTTGACCTGGATGAA 371
Db          49 LeuGlnAspMetIleAsnGluValAspAlaAspGlyAsnGlyThrIleGluPheValGlu 68
Oy          370 TTCTTGTTCTTTATGAATCCATCTCGAACCACTGGCAGCAATGGTGTGACGAAGAGAG 311
Db          69 PheLeu-----AsnLeuMetAlaLysLysMetLysGluThrAsp 81
Oy          310 GAGAGGAATTTGTCATTCACGGCGCGCGGTGAAGAAAGACATGACCTTGGCGAAGCT 251
Db          82 GluGluGlu-----AspLeuLysGluAla 89
Oy          250 TTTAAGTGTGACTTGATGAGGATGGGATGGGAGATGTGAGAGCTTGAATTACGTT 191
Db          90 PheLysValPheAspLysAspGlnAsnGlyYrIleSerAlaSerGluLeuArgHisVal 109
Oy          190 CTGGGAACAACGCGGATATGTGAGCTGAAGAAATAGTGAAGAAAGACTGAGAGCATGATTGG 131
Db          110 MetIleAsnLeuGly-----GluLysLeuThrAspGluGluValGluGlnMetIleGlu 127

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Cy 130 TATTACGACACCAATTGACGGCGATGGTGTATTTCGAAGATTCAGAAACATGATGTTA 71
Db 128 GUAAlAspLeuAspGlyAspGlyGlnValAsnTyrAspGlnPheValLysMetMetMet 147

RESULT 8
US-08-818-253-2
: Sequence 2, Application US/08818253
: Patent No. 5998264
: GENERAL INFORMATION:
: APPLICANT: Tsien, Roger Y.
: APPLICANT: Miyawaki, Atsushi
: TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
: TITLE OF INVENTION: DETECTION OF ANALYTES
: NUMBER OF SEQUENCES: 61
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson P.C.
: STREET: 4225 Executive Square, Suite 1400
: CITY: La Jolla
: STATE: CA
: COUNTRY: USA
: ZIP: 92037
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: Windows 95
: SOFTWARE: FastSeq for Windows Version 2.0b
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/818,253
: FILING DATE: 14-MAR-1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Halle, Ph.D., Lisa A.
: REGISTRATION NUMBER: 38,347
: REFERENCE/DOCKET NUMBER: 07257/043001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619/678-5070
: TELEFAX: 619/678-5099
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 642 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: FRAGMENT TYPE: internal
:
US-08-818-253-2

Alignment Scores:
Pred. No.: 2,39e-08 Length: 642
Score: 147.00 Matches: 41
Percent Similarity: 50.66% Conservative: 36
Best Local Similarity: 26.97% Mismatches: 57
Query Match: 13.85% Indels: 18
DB: 2 Gaps: 4

US-10-021-323-13 (1-609) * US-08-818-253-2 (1-642)
Cy 526 GACTTGCAACGCGTATTGCAGAACTGCAGCAAGATGAGATGGCTTCGTTAGCTGGAG 467
Db 241 GlnPheLysGlnAlaPheSerLeuPheAspGlyAspGlyThrIleThrLys 260
Cy 466 GAGCTGAATTGGTGTCTGCAGAGATCCGAGTCTGTCCAATTCAGCCTTGAA--GAATTG 410
Db 261 GlnGlnGlyThrValMetArgSerLeuLys-----GlnAsnProThrGlnAlaGlnLeu 278
Cy 409 GAGCCCTTAGTGGGAGAAACCATGTTGAACCTTGATGATGTAATCTGTCTTTATGAATCC 350
Db 279 GlnAspMetLysAsnGlnValAlaPheAlaAspGlyAsnGlyThrIleTyrPheProGlnPhe 298
Cy 349 ATCTGCAACCCACTGCGACATGCTGCTGTCACGAAGACGAGAGAGGAATGGTCATTCAC 250
Db 299 LeuThrMetMetAlaArgLysMetLysAspThrAspSerGlnGlnGlu----- 314

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OY 289 GCGGCGGTGAAGAGACAGTGCCTTGCGAAGCTTTTAAGTGTTCAGTTGAT 230
DB 315 -----11eargglua1aPhearValPheaspIysasp 325
OY 229 GCGGATGGGTGGGGGATGTAGAGCTTGAATACGTCTGGGAGAACTGGGTATGTA 170
DB 326 G1Yanng1Yr11eser1a1aGluea1aRgh1seValMetThrasnleugly----- 343
OY 169 GGTGAANAATGTAAGAAACAGTCGAGAGCATGATTTGTATTAGACCAATTCCAGAC 110
DB 344 G1u1y1e1u1Thrasp1u1a1a1asp1u1e11eargglua1a1asp1u1yasp 363
OY 109 GCGATGTTGATTTTCAGAAATTCAAAACATGATG 74
DB 364 G1yG1n1va1a1n1tyr1g1u1n1p1h1e1a1G1n1u1e1m1e1t 375

RESULT 9
US-08-818-252-2
; Sequence 2, Application US/08818252B
; Patent No. 6197928
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; FILE REFERENCE: 07257/042001
; CURRENT APPLICATION NUMBER: US/08/818,252B
; FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 642
; TYPE: PRP
; ORGANISM: Meguorea victoria
US-08-818-252-2

Alignment Scores:
Pred. No.: 2,39e-08 Length: 642
Score: 147.00 Matches: 41
Percent Similarity: 50.66% Conservative: 36
Best Local Similarity: 26.97% Mismatches: 57
Query Match: 13.85% Indels: 18
DB: 3 Gaps: 4

US-10-021-323-13 (1-609) x US-08-818-252-2 (1-642)
OY 526 GACTTGCAACGCGATTCGAGAAAGCTCGACAAAGATGAGATGCTTCGTAGCTGAG 467
DB 241 GluPhelysGluAlaPheaserLeuPheaspIysaspGlyThrIleThrThryls 260
OY 466 GAGCTGAATGTTGCTCCAGAGATCGGCTCTGCCAATTACGCTTGA---GAATTG 410
DB 261 GluLeuGlyThrValMetArgserLeuGly-----GlnasnProthrGluAlaGluLeu 278
OY 409 GAGCCCTTAGTGGGAAACCATGTTGAACCTTGATGATTCGTTGCTTTATGATCC 350
DB 279 GlnaspMetIleasnGluValaspAlaaspGlyasnGlyThrIleTyrrheProGluPhe 298
OY 349 ATCTGAAACCACTGGACATGTGTGTGACGAAGAGAGAGAGAGAAATGTCATTCC 290
DB 299 LeuThrMetMetAlaArglyMetIysaspThrIaspserGluGlu----- 314
OY 289 GCGGCGGTGAAGAAACAGTCAGCTTCGGAAGGCTTTAAAGTGTTCAGTTGAT 230
DB 315 -----11eargglua1aPhearValPheaspIysasp 325
OY 229 GCGGATGGGTGGGGGATGTAGAGCTTGAATACGTCTGGGAGAACTGGGTATGTA 170
DB 326 G1Yanng1Yr11eser1a1aGluea1aRgh1seValMetThrasnleugly----- 343
OY 169 GGTGAANAATGTAAGAAACAGTCGAGAGCATGATTTGTATTAGACCAATTCCAGAC 110
DB 344 G1u1y1e1u1Thrasp1u1a1a1asp1u1e11eargglua1a1asp1u1yasp 363
DB 364 G1yG1n1va1a1n1tyr1g1u1n1p1h1e1a1G1n1u1e1m1e1t 375

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DB 344 Glu1y1e1u1Thrasp1u1a1a1asp1u1e11eargglua1a1asp1u1yasp 363
OY 109 GCGATGTTGATTTTCAGAAATTCAAAACATGATG 74
DB 364 G1yG1n1va1a1n1tyr1g1u1n1p1h1e1a1G1n1u1e1m1e1t 375

RESULT 10
US-08-818-253-4
; Sequence 4, Application US/08818253
; Patent No. 5988204
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; FILE REFERENCE: 07257/043001
; CURRENT APPLICATION NUMBER: US/08/818,253
; FILING DATE: 14-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07257/043001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 652 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-818-253-4

Alignment Scores:
Pred. No.: 2,41e-08 Length: 652
Score: 147.00 Matches: 41
Percent Similarity: 50.66% Conservative: 36
Best Local Similarity: 26.97% Mismatches: 57
Query Match: 13.85% Indels: 18
DB: 2 Gaps: 4

US-10-021-323-13 (1-609) x US-08-818-253-4 (1-652)
OY 526 GACTTGCAACGCGATTCGAGAAAGCTCGACAAAGATGAGATGCTTCGTAGCTGAG 467
DB 241 GluPhelysGluAlaPheaserLeuPheaspIysaspGlyThrIleThrThryls 260
OY 466 GAGCTGAATGTTGCTCCAGAGATCGGCTCTGCCAATTACGCTTGA---GAATTG 410
DB 261 GluLeuGlyThrValMetArgserLeuGly-----GlnasnProthrGluAlaGluLeu 278
OY 409 GAGCCCTTAGTGGGAAACCATGTTGAACCTTGATGATTCGTTGCTTTATGATCC 350
DB 279 GlnaspMetIleasnGluValaspAlaaspGlyasnGlyThrIleTyrrheProGluPhe 298
OY 349 ATCTGAAACCACTGGACATGTGTGTGACGAAGAGAGAGAGAGAAATGTCATTCC 290

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DB 229 LeuThrMetMetAlaArglyMetlysaBpThrAspSerGluGlu----- 314
QY 289 GGGGGCGGGAAGAGAAGAACAGTACCTTGGCAAGCTTTAAAGCTTTGACCTTGAT 230
DB 315 -----11eaAgGluAlaPheArgValPheAspLysAsp 325
QY 229 GGGGATGGGTGGGGGATGTGAGAGCTTGATACCTGCTGGGAAGACTGGGATATGTA 170
DB 326 G1yaenglyTyrlleSerAlaAlaGluLeuAArgHleValMetThrAsnleuGly----- 343
QY 169 GGTGAATAAGTGAAGAAAGACTGCAGAGCATGATTTGGTATTACGACCAATTTCAGAC 110
DB 344 G1uylsLeuThrAspGluGluValAspGluMetlleArgGluAlaAsp11leaSpGlyAsp 363
QY 109 GGCATGTTGATTTTCAGAAATTCAAAAACATGATG 74
DB 364 GlyGlnValAsnTyrlGluGluPheValGlnMetMet 375

RESULT 11

US-08-818-252-4
Sequence 4, Application US/08818252B
Patent No. 6187928
GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
FILE REFERENCE: 07257/042001
CURRENT APPLICATION NUMBER: US/08/818,252B
CURRENT FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 652
TYPE: PRT
ORGANISM: Aequorea victoria
US-08-818-252-4

Alignment Scores:

Pred. No.:	2,41e-08	Length:	652
Score:	147.00	Matches:	41
Percent Similarity:	50.66%	Conservative:	36
Best Local Similarity:	26.97%	Mismatches:	57
Query Match:	13.85%	Indels:	18
DB:	3	Gaps:	4

US-10-021-323-13 (1-609) x US-08-818-252-4 (1-652)

QY 526 GACTTGCAACGGGTATTGCAAGACCTCGAAGAAATGAGATGGCTTCTAGTCGAG 467
DB 241 GuupheLySGluAlaPheSerleuPheAspLyAspGlyAspGlyThrIleThrThrLys 260
QY 466 GAGCTGAATGGTGTCTCCAGAGAAATCGGCTGTCTCCAAATTCAGCCTTGAA--GAATTG 410
DB 261 G1uLeuGlyThrValMetArgSerleuGly-----GlnAsnProthrGluAlaGluLeu 278
QY 409 GAGCCCTTAGTGGGAAAAACCATGTTGAACCTTGATGAATCTTGTCTTTATGATCC 350
DB 279 GlnAspMetCileAsnGluValAspAlaAspGlyAsnGlyThrIleTyrlPheProGluPhe 298
QY 349 AACTGGAACCCACTGSCACATGCTGTGTGACGAAGAGAGAGAGAGATGTCATTGAC 290
DB 299 LeuThrMetMetAlaArglyMetlysaBpThrAspSerGluGluGlu----- 314
QY 289 GCGCGGATGAAGAGAAGACAGTGAACCTTGCAAGAGCTTTAAAGTGTGTTGATTCAT 230
DB 315 -----11eaAgGluAlaPheArgValPheAspLysAsp 325
QY 229 GGGGATGGGTGGGGGATGTGAGAGCTTGATACCTGCTGGGAAGACTGGGATATGTA 170
DB 326 G1yaenglyTyrlleSerAlaAlaGluLeuAArgHleValMetThrAsnleuGly----- 343

QY 169 GGTGAATAAGTGAAGAAAGACTGCAGAGCATGATTTGGTATTACGACCAATTTCAGAC 110
DB 344 G1uylsLeuThrAspGluGluValAspGluMetlleArgGluAlaAsp11leaSpGlyAsp 363
QY 109 GGCATGTTGATTTTCAGAAATTCAAAAACATGATG 74
DB 364 GlyGlnValAsnTyrlGluGluPheValGlnMetMet 375

RESULT 12

US-08-464-164-2
Sequence 2, Application US/08464164
Patent No. 5614195
GENERAL INFORMATION:
APPLICANT: Tomley, Fiona M.
APPLICANT: Dunn, Paul P. J.
APPLICANT: Bumstead, Janene M.
APPLICANT: Vermeulen, Arno N.
TITLE OF INVENTION: Coccidiosis poultry vaccine
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Akzo No. 5614195el Patent Department
STREET: 1300 Piccard Drive, Suite 206
CITY: Rockville
STATE: Maryland
COUNTRY: U.S.A.
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,164
FILING DATE: June 2, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gormley, Mary E.
REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 258-5200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 456 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-164-2

Alignment Scores:

Pred. No.:	3.08e-08	Length:	456
Score:	145.50	Matches:	51
Percent Similarity:	41.18%	Conservative:	26
Best Local Similarity:	27.27%	Mismatches:	59
Query Match:	13.71%	Indels:	51
DB:	1	Gaps:	6

US-10-021-323-13 (1-609) x US-08-464-164-2 (1-456)

QY 565 ATCTCTTGTGGTGAATATGTCCTCCCTTAGTAAGACCGAC--TTGCAACGCGTATTC 509
DB 290 LeuTyrlMetGlySerlyLeuThrThrAsnGluGluThrAspGluLeuAsnLysIlePhe 309
QY 508 GAGAACTCGACAAAGATAGAGATGGCTTGTAGTCTGAGAGACTGAATTGGTTCCTC 449
DB 310 G1uylsMetAspLyAsnGlyAspGlyGlnLeuAspLyGlnGluLeu----- 325
QY 448 CAGAGAATCGGCTGTGCAATTGACCTTGGAAGATTGAGACCTTGTGGGAACA 389
DB 326 -----MetGluGlyTyrlValGluLeuMetlysaBpLysGlyGluAsp 339
QY 388 TGTTTGAATCGATGAATCTTGTGTTTATGAATCCATCTCGAACCACCTGCACAT 329
DB 340 ValSerValLeuAspLysSerAlaIle----- 348

QY 328 GGTGTGACGAAGAGAGAGAAATGTCATTACAGC-----GGC 284
DB 349 -----GluThrGluValGluGluValLeuGluValAlaAspPheAspLysAsn 364
QY 283 GGTGAAGAAGAACAGTGAC----- 263
DB 365 GllPheIleGluTyrSerGluPheValThrValAlaMetAspArgArgThrLeuSer 384
QY 262 -----CTTGCAAGCTTTTAAAGCTTTGACTGAAATGGGAGATGGTGGGGGA 212
DB 385 ArgGlnArgLeuGlnArgAlaPheGluMetPheAspSerAspGlySerGlyLysIleSer 404
QY 211 TGTGAGAGCTTGAAATACGTCTGGAGAGACTGGGTATGTGAGAAATAGTGAAA 152
DB 405 SerSerGluLeuAlaThrIlePheGlyVal-----SerGluLeuAspSerGlu 420
QY 151 GACTGCAGAGCAGATGTTGTAATACGACACCAATTCAGACGCGATGGTTGATTC 92
DB 421 AlaTPrArgArgValLeuAlaGluValAlaAspArgAsnAspGlyGluValAspPheGlu 440
QY 91 GAATTCAAAACATGATGTTA 71
DB 441 GluPheGlnGlnMetLeuLeu 447
RESULT 13
US-08-338-057-2
; Sequence 2, Application US/08338057
; Patent No. 5795741
; GENERAL INFORMATION:
; APPLICANT: Tomley, Fiona M.
; APPLICANT: Dunn, Paul P. J.
; APPLICANT: Bumstead, Janene M.
; APPLICANT: Vermeulen, Arno N.
; TITLE OF INVENTION: Coccidiosis poultry vaccine
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Organon Teknika Corporation
; STREET: 1330 Piccard Drive
; CITY: Rockville
; STATE: Maryland
; COUNTRY: U.S.A.
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/338,057
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93.309078.9
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Gornley, Mary E.
; REGISTRATION NUMBER: 34,409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 258-5200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 456 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-338-057-2
Alignment Scores:
Pred. No.: 3.08e-08 Length: 456
Score: 145.50 Matches: 51
Percent Similarity: 41.18% Conservative: 26
Best Local Similarity: 27.27% Mismatches: 59

Query Match: 13.71% Indels: 51
DB: 1 Gaps: 6
US-10-021-323-13 (1-609) x US-08-338-057-2 (1-456)
QY 565 ATCTCTTGTGTGTAATAATGCCCTTGTAGTAAGACCGC---TTGCAACGGTATTC 509
DB 290 LeuTyrMetGlySerLysLeuThrThrAsnGluThrAspGluLeuValAsnLysIlePhe 309
QY 508 GAGAAGCTCGACAGAATATGATAGCTTCTGTAGTCGTGAGAGCTGAAATTTGTTGCTC 449
DB 310 GlnLysMetAspLysAsnGlyAspGlyGluLeuAspLysGlnGluLeu----- 325
QY 448 CAGAGAATCGGCTGTCCATTCACGCTTGAAGAAATGGAGCCCTTGGGAAAACCA 389
DB 326 -----MetGluGlyTyrValGluLeuMetLysLeuLysGlyGluAsp 339
QY 388 TGTTTGAACCTTGATGAATCTTCTTTTATGAAATTCATCTGAAACCACTGGACAT 329
DB 340 ValSerValLeuAspLysSerAlaIle----- 348
QY 328 GGTGTGACGAAGAGAGAGAGAAATTTGTCATTACAGC-----GGC 284
DB 349 -----GluThrGluValGluGluValLeuGluValAlaAspPheAspLysAsn 364
QY 283 GGTGAAGAAGAACAGTGAC----- 263
DB 365 GlyPheIleGluTyrSerGluPheValThrValAlaMetAspArgArgThrLeuSer 384
QY 262 -----CTTGCAAGCTTTTAAAGCTTTGACTGAAATGGGAGATGGTGGGGGA 212
DB 385 ArgGlnArgLeuGlnArgAlaPheGluMetPheAspSerAspGlySerGlyLysIleSer 404
QY 211 TGTGAGAGCTTGAAATACGTCTGGAGAGACTGGGTATGTGAGTGAATAATAGTGAAA 152
DB 405 SerSerGluLeuAlaThrIlePheGlyVal-----SerGluLeuAspSerGlu 420
QY 151 GACTGCAGAGCAGATGTTGTAATACGACACCAATTCAGACGCGATGGTTGATTC 92
DB 421 AlaTPrArgArgValLeuAlaGluValAlaAspArgAsnAspGlyGluValAspPheGlu 440
QY 91 GAATTCAAAACATGATGTTA 71
DB 441 GluPheGlnGlnMetLeuLeu 447
RESULT 14
US-08-668-416-2
; Sequence 2, Application US/08668416
; Patent No. 5843722
; GENERAL INFORMATION:
; APPLICANT: Tomley, Fiona M.
; APPLICANT: Dunn, Paul P. J.
; APPLICANT: Bumstead, Janene M.
; APPLICANT: Vermeulen, Arno N.
; TITLE OF INVENTION: Coccidiosis poultry vaccine
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akzo No. 5843722el Patent Department
; STREET: 1300 Piccard Drive, Suite 206
; CITY: Rockville
; STATE: Maryland
; COUNTRY: U.S.A.
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/668,416
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

Mon Feb 2 08:52:48 2004

us-10-021-323-13.rtf

Page 10

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Oy 109 GGCATGGTGTGATTTCACGAATTCAAAAACATGATGTTA 71
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Db 135 GlyI nValAsnTy rGlu nIup nValArg m e tMetLeu 147

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Search completed: January 31, 2004, 02:43:44
Job time : 22.5 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: January 31, 2004, 02:32:26 ; Search time 44.5 Seconds

(without alignments)
5668.308 Million cell updates/sec

Title: US-10-021-323-13

Perfect score: 1100

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Scoring table:
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Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 769580 segs, 207824079 residues

Total number of hits satisfying chosen parameters: 1579160

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-O=/cgn2_1/USPTO_epool/US10021323/runat_30012004_112102_3623/app.query.fasta_1.775
-DB=Published Applications AA -OFMT=faa -SUFFIX=rapb -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=plc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10021323@cgn_1.1.46@runat_30012004_112102_3623
-NCPU=6 -ICPU=3 -NO_MMAP -LANG=QUEERY -NEG_SCORES=0 -WAIT -OSBLOCK=100
-LONGIOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PTC_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PTCT5_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 1	239.5	22.6	205	11	US-09-847-208-45	Sequence 45, Appl
C 2	204	19.2	145	12	US-10-369-493-5397	Sequence 5397, Ap
C 3	154	14.5	159	10	US-09-910-071-5	Sequence 5, Appl
C 4	152.5	14.4	160	12	US-10-176-416-1	Sequence 1, Appl
C 5	152.5	14.4	160	15	US-10-192-806-1	Sequence 1, Appl
C 6	152.5	14.4	160	15	US-10-286-134-1	Sequence 1, Appl
C 7	152	14.3	150	12	US-10-369-493-6776	Sequence 6776, Ap
C 8	147	13.9	642	10	US-09-554-000-2	Sequence 2, Appl
C 9	147	13.9	652	10	US-09-554-000-4	Sequence 4, Appl
C 10	146.5	13.8	218	12	US-10-369-493-6535	Sequence 6535, Ap
C 11	144	13.6	642	10	US-09-554-000-6	Sequence 6, Appl
C 12	144	13.6	656	10	US-09-554-000-8	Sequence 8, Appl
C 13	143	13.5	408	11	US-09-988-462-21	Sequence 21, Appl
C 14	143	13.5	464	11	US-09-988-462-22	Sequence 22, Appl
C 15	142	13.4	464	12	US-10-369-493-6260	Sequence 6260, Ap
C 16	142	13.4	416	11	US-09-989-025A-4	Sequence 8, Appl
C 17	141	13.3	148	11	US-09-989-025A-4	Sequence 4, Appl
C 18	141	13.3	149	12	US-10-341-434-105	Sequence 105, App
C 19	141	13.3	149	15	US-10-291-172-219	Sequence 219, App
C 20	141	13.3	149	15	US-10-177-293-35	Sequence 35, Appl
C 21	139.5	13.1	227	12	US-10-291-172-243	Sequence 243, Appl
C 22	138	13.0	136	12	US-10-342-324-60	Sequence 60, Appl
C 23	136.5	12.9	142	10	US-09-910-071-4	Sequence 4, Appl
C 24	136.5	12.9	957	12	US-10-259-165-252	Sequence 252, App
C 25	136	12.8	187	12	US-10-369-493-2146	Sequence 2146, Ap
C 26	132.5	12.5	187	12	US-10-259-165-4	Sequence 4, Appl
C 27	132.5	12.5	187	12	US-10-259-165-358	Sequence 358, App
C 28	132	12.4	142	11	US-09-988-462-24	Sequence 24, Appl
C 29	130.5	12.3	501	12	US-10-289-172-3	Sequence 3, Appl
C 30	130.5	12.3	501	12	US-09-848-806-3	Sequence 3, Appl
C 31	128.5	12.1	163	11	US-09-764-881-126	Sequence 126, App
C 32	128.5	12.1	163	12	US-10-242-747-126	Sequence 126, App
C 33	128.5	12.1	163	12	US-10-158-057-305	Sequence 305, App
C 34	127.5	12.0	146	15	US-10-157-031-295	Sequence 295, App
C 35	127	12.0	160	12	US-10-369-493-5550	Sequence 5550, App
C 36	123	11.6	141	12	US-10-369-493-19795	Sequence 19795, A
C 37	121.5	11.5	163	12	US-10-320-797-3020	Sequence 3020, Ap
C 38	121.5	11.5	495	12	US-10-289-172-1	Sequence 1, Appl
C 39	121.5	11.5	495	12	US-09-848-806-1	Sequence 1, Appl
C 40	120.5	11.4	371	12	US-10-353-826-9	Sequence 9, Appl
C 41	120.5	11.4	390	12	US-10-353-826-4	Sequence 4, Appl
C 42	118	11.1	639	10	US-09-854-731-17	Sequence 17, Appl
C 43	117.5	11.1	167	15	US-10-128-714-8159	Sequence 8159, Ap
C 44	117	10.6	258	12	US-10-104-047-3034	Sequence 3034, Ap
C 45	117	11.0	549	12	US-10-259-194A-258	Sequence 258, App

ALIGNMENTS

RESULT 1
US-09-847-208-45
; Sequence 45, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhu, Daocheng
; APPLICANT: Zhang, Ke
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67.002A
; CURRENT APPLICATION NUMBER: US/09/847.208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Betula verrucosa (White birch) (Betula pendula)
US-09-847-208-45

Alignment Scores: 1.73e-16 Length: 205
Pred. No.: 239.50 Matches: 63
Score:

Percent Similarity:	57.93%	Conservative:	32
Best Local Similarity:	38.44%	Mismatches:	58
Query Match:	22.57%	Indels:	11
DB:	11	Gaps:	6

US-10-021-323-13 (1-609) X US-09-847-208-45 (1-205)

Oy 538 CTTAGTAAAGACCACGACTTGCACACGCTATTCGAGAGCTCCAGAAATGAGATGGCTTC 479
 Db 36 LeuAenThlrLeuAargLeuAArgIlePheAspLeuAeApLyAaenSerAspClylle 55
 Oy 478 GTTAGCTCTGAGAGAGCTGGAATGGTCTCCAGAAATCGGAGTCTGTCCAATTACGCTT 419
 Db 56 IleThnValAspLileuSerArgAlaLeuAenLeuGly--LeuGluThrAspLeu 74
 Oy 418 GAAGAATTGAGCCCTTAGTG-----GGAAACCATGTTTGAACTTG 377
 Db 75 SerGluLeuGluSerThrValLySerPheThrArgGluGluAanIleGlyLeuGluPhe 94
 Oy 376 GATGAATCTTGTCTTTATGAATCCATCCAGAACCA---CTGGACACATGGTGT--- 323
 Db 95 GluAspPheIleSerLeuHisGlnSerLeuAsnAspSerLyrrPheAlaTyrglyGlyGlu 114
 Oy 322 GACGAAGAGGAGGAGAGCAATTGGTCATTCACGCCGCGGTGAAGAAAGACAGATGAC 263
 Db 115 AspGluAspAspAsnGluGluAspMetAryLySerIleuSerGlnGluGluAsp 134
 Oy 262 CTTGCGAAGGCTTTAAAGTGTTCGACTTGAATGGGATGGGCTGGGGGAGATGTGACAG 203
 Db 135 SerPheGlyGlyPheLySerValPheAspGluAspGlyTyrrIleSerAlaArgIlu 154
 Oy 202 CTTGATAGCTGCTGGGAGACCTGGCGATATGTGAGAGTGAATAATGTGAAAAGAC---TGC 146
 Db 155 LeuGlnMetValLeuGlyLyLeuGlyPhe--SerGluGlySerGluIleAspArgVal 173
 Oy 145 AGGAGCATGATTTGTATTACGACACCAATTCACGCGCATGTGTGATTTTCAAGATTC 86
 Db 174 GluLySerMetIleValSerValAspSerAsnAryAspGlyAryGluValAspPhePheGluPhe 193
 Oy 85 AAAAACATGATG 74
 Db 194 LyAspMetMet 197

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RESULT 2
US-10-369-493-5397
; Sequence 5397, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369, 493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360, 039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5397
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5397

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Alignment Scores:	
Pred. No.:	8.99e-13
Score:	204.00
Percent Similarity:	52.12%
Best Local Similarity:	30.30%
Query Match:	19.23%
Length:	145
Matches:	50
Conservative:	36
Mismatches:	49
Indels:	30

DB:	12	Gaps:	5
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US-10-021-323-13 (1-609) X US-10-369-493-5397 (1-145)

[illegible]

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RESULT 3
US-09-910-071-5
; Sequence 5, Application US/09910071
; Patent No. US20020116146A1
; GENERAL INFORMATION:
; APPLICANT: Tomikawa, Mayumi
; APPLICANT: Aikawa, Seichi
; APPLICANT: Matsuzawa, Fumiko
; TITLE OF INVENTION: Method and Apparatus for Extracting and Evaluating Mutually Similar
; TITLE OF INVENTION: Portions in One-Dimensional Sequences in Molecules and/or Three
; TITLE OF INVENTION: Structures of Molecules
; FILE REFERENCE: 522.1921D2
; CURRENT APPLICATION NUMBER: US/09/910,071
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 08/014,867
; PRIOR FILING DATE: 1993-02-08
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 159
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: Figure 23B
US-09-910-071-5

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Alignment Scores:	
Pred. No.:	1.83e-07
Score:	154.00
Percent Similarity:	45.22%
Best Local Similarity:	28.03%
Query Match:	14,518
DB:	10
Length:	159
Matches:	44
Conservative:	27
Mismatches:	60
Indels:	5
Gaps:	26

US-10-021-323-13 (1-609) x US-09-910-071-5 (1-159)

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QY 526 GACCTGCAACGGGTATTCGAGAGCTCGACAGAAATGAGATGCTTGTGCTGAG 467
DB 19 GlnPheLysAlaAlaPheAspMetPheAspAlaAspGlyGlyAspIleSerThrLys 38
QY 466 GAGCTGAATGGTGTCTCCAGAGATCGGGTCTGTCCATTCAGCTTGAAGAAATGGAG 407
DB 39 GluLeuGlyThrValMetArgMetLeuGlyGln---AsnProThrLysGluGluLeuAsp 57
QY 406 CCCTTAGTG-----GAAAAACATGTTGAATCTTGATGAATCTTG 365
DB 58 AlaIleIleGluGluValAspGluAspGlySerGlyThrIleAspPheGluGluPheLeu 77
QY 364 TTCCTTTAATGATCCATCTCGAACCCACTGCGACATGTGTGTGAGAGAGAGAGAG 305
DB 78 ValMetValArgGluMetLysGluAsp---AlaLysGlyLysSerGluGluGln----- 94
QY 304 GAATTGTCATTCAACGGCGCGGTGAAGAAAGACAGTGAACCTTGCGAAGGCTTTAA 245
DB 95 -----LeuAlaAspCysPheArg 100
QY 244 GTGTTGACTTGAATGCGGATGCGGTGGCGGATGTGAGAGCTTGAATACGTCGTGGA 185
DB 101 IlePheAspLysAsnAlaAspGlyPheIleAspIleGluGluLeuGlyGluIleLeuArg 120
QY 184 AGACTGGGTATGTGAGCTGAAAAATAGTGAAGAAAGACTGAGAGCATGATTGCTATTAC 125
DB 121 AlaThrGly-----GluHisValThrAspGluGluIleGluAspLeuMetLysAspSer 138
QY 124 GACCAATTCAGACGGCATGCTGATTTTCAGAAATTCAAAAACATGATG 74
DB 139 AspLysAsnAsnAspGlyArgIleAspPheAspGluPheLeuLysMetMet 155

RESULT 4
US-10-176-416-1
; Sequence 1, Application US/10176416
; Publication No. US20030186864A1
; GENERAL INFORMATION:
; APPLICANT: Thorm, R.
; APPLICANT: Lanzer, M.
; APPLICANT: Moses, M.
; APPLICANT: Wiederschain, D.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING TROPONIN SUBUNITS,
; TITLE OF INVENTION: INHIBIT ANGIOGENESIS
; FILE REFERENCE: 8657-043
; CURRENT APPLICATION NUMBER: US/10176,416
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 09/442,099
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/268,274
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: 08/961,264
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: 08/602,941
; PRIOR FILING DATE: 1996-02-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-176-416-1

Alignment Scores:
Pred. No.: 2,65e-07 Length: 160
Score: 152.50 Matches: 43
Percent Similarity: 45.86% Conservative: 29
Best Local Similarity: 27.39% Mismatches: 60
Query Match: 14.37% Indels: 25
DB: 12 Gaps: 4

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US-10-021-323-13 (1-609) x US-10-176-416-1 (1-160)

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QY 526 GACCTGCAACGGGTATTCGAGAGCTCGACAGAAATGAGATGCTTGTGCTGAG 467
DB 19 GlnPheLysAlaAlaPheAspMetPheAspAlaAspGlyGlyAspIleSerThrLys 38
QY 466 GAGCTGAATGGTGTCTCCAGAGATCGGGTCTGTCCATTCAGCTTGAAGAAATGGAG 407
DB 39 GluLeuGlyThrValMetArgMetLeuGlyGlnThrPro---ThrLysGluGluLeuAsp 57
QY 406 CCCTTAGTG-----GAAAAACATGTTGAATCTTGATGAATCTTG 365
DB 58 AlaIleIleGluGluValAspGluAspGlySerGlyThrIleAspPheGluGluPheLeu 77
QY 364 TTCCTTTAATGATCCATCTCGAACCCACTGCGACATGTGTGTGAGAGAGAGAGAG 305
DB 78 ValMetValArgGluMetLysGluAspAlaLysGlyLysSerGluGluGln----- 95
QY 304 GAATTGTCATTCAACGGCGCGGTGAAGAAAGACAGTGAACCTTGCGAAGGCTTTAA 245
DB 96 -----LeuAlaGluCysPheArg 101
QY 244 GTGTTGACTTGAATGCGGATGCGGTGGCGGATGTGAGAGCTTGAATACGTCGTGGA 185
DB 102 IlePheAspArgAsnAlaAspGlyThrIleAspProGluGluLeuAlaGluIlePheArg 121
QY 184 AGACTGGGTATGTGAGCTGAAAAATAGTGAAGAAAGACTGAGAGCATGATTGCTATTAC 125
DB 122 AlaSerGly-----GluHisValThrAspGluGluIleGluSerLeuMetLysAspGly 139
QY 124 GACCAATTCAGACGGCATGCTGATTTTCAGAAATTCAAAAACATGATG 74
DB 140 AspLysAsnAsnAspGlyArgIleAspPheAspGluPheLeuLysMetMet 156

RESULT 5
US-10-192-806-1
; Sequence 1, Application US/10192806
; Publication No. US20030083255A1
; GENERAL INFORMATION:
; APPLICANT: Thorm, R.
; APPLICANT: Lanzer, M.
; APPLICANT: Moses, M.
; APPLICANT: Wiederschain, D.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING
; TITLE OF INVENTION: TROPONIN SUBUNITS, FRAGMENTS AND HOMOLOGS THEREOF AND
; TITLE OF INVENTION: METHODS OF THEIR USE TO INHIBIT ANGIOGENESIS
; FILE REFERENCE: 8657-042-999
; CURRENT APPLICATION NUMBER: US/10192,806
; CURRENT FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: 09/612,421
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/268,274
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: 08/961,264
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: 08/602,941
; PRIOR FILING DATE: 1996-02-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-192-806-1

Alignment Scores:
Pred. No.: 2,65e-07 Length: 160
Score: 152.50 Matches: 43
Percent Similarity: 45.86% Conservative: 29
Best Local Similarity: 27.39% Mismatches: 60
Query Match: 14.37% Indels: 25
DB: 15 Gaps: 4

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Db      53 SerProthGluAspGluLeuAspAlaMetPheGlnAlaAlaAspIleAspGly 72
Qy      385 ---TTGACCTGGATTAATCTTCTTATGATTCATCGAACCACTGGACAT 329
      73 AenIleAspPheGlnIleLeuValIleAlaIleS---AlaAsnProLeuSer--- 89
Qy      328 GGTGTGACGAAGAGAGAGAGGAATGTTCATTCACGGCGCGGTGAAGAAGAGAC 269
      89 -----
Qy      268 AGTGACCTTGACAGGCTTTTAAGTCTTGACTTCATGCGGATGGTGGGGGATGT 209
      90 LeuSerLeuIleValAlaValPheGlnGluLeuAspValAspGlyIleThrArg 109
Qy      208 GAGGACCTGATACCTGCTGGAGAGCTGGGATGTGAGGTAATAATGTGAAAGAC 149
      110 SerGluLeuArgThrAlaPheGlnArgMetGly-----HisSerLeuSerAspGlnAsp 127
Qy      148 TGCAGAGACATGATTTGTATTAACGACCAATTCAGACGCGATGTTGATTTCA 92
      128 IleValAlaIleTyrArgHisValAspGlnAsnAsnAspGlyLysIleAsnPheGln 146

RESULT 8
US-09-554-000-2
; Sequence 2, Application US/09554000
; Patent No. US20020165364A1
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; FILE REFERENCE: 07257/042001
; CURRENT APPLICATION NUMBER: US/09/554,000
; PRIORITY FILING DATE: 2000-04-20
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 642
; TYPE: PR
; ORGANISM: Aequorea victoria
US-09-554-000-2

Alignment Scores:
Pred. No.:      1,586-06      Length:      642
Score:          147.00      Matches:      41
Percent Similarity: 50.66%      Conservative: 36
Best Local Similarity: 26.97%      Mismatches: 57
Query Match:    13.85%      Indels:      18
DB:            10      Gaps:      4

US-10-021-323-13 (1-609) x US-09-554-000-2 (1-642)
Qy      526 GACTTCAACGCGTATTTCGAGAAGCTCGACAAATGAGATGCTTGTATGCTGAG 467
      241 GiuphelyGluAlaPheSerLeuPheAspIleAspGlyThrIleThrArgLys 260
Qy      466 GAGCTGAATGTGCTTCAGAGAAATCGGCTCTGTCCAATTCAGCCTTGAA---GAATTG 410
      261 GluLeuGlyThrValMetArgSerLeuGly-----GlnAsnProThrGlnAlaGluLeu 278
Db      409 GAGCCTTAGTGGGAAACATCTTGAACCTTGAGATTCCTGCTTTATGATTC 350
      279 GlnAspMetIleAsnGluValAspAlaAspGlyAsnGlyThrIleThrArgProGluPhe 298
Qy      349 ATCTGAAACCACTGCGACATGCTGTGACGAAGAGAGAGAGGAATGTGTCATTGAC 290
      299 LeuThrMetMetAlaArgLysMetLysAspThrAspSerGluGluGlu----- 314
Qy      289 GGGCGGCGTGAAGAAGAGACATGACCTTGCGAAGGCTTTTAAGTGTGCTTGAT 230
      289 GGGCGGCGTGAAGAAGAGACATGACCTTGCGAAGGCTTTTAAGTGTGCTTGAT 230
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Db      315 -----IleArgGluAlaPheArgValPheAspIleAsp 325
Qy      229 GGGATGGTGGGGGAGATGTGAGAGCTTGAATACGTGCTGGAAAGACTGGTATGCA 170
      326 GlnAsnGlyTyrIleSerAlaAlaGluLeuArgHisValMetThrAsnLeuGly----- 343
Qy      169 GGTGAATAATAGTGAAGAAAGACTGCGAGAGCATGATTTGTGATTAACACCAATTGAGAC 110
      344 GluLysLeuThrAspGluGluValAlaAspGluMetIleArgGluAlaAspIleAspGlyAsp 363
Db      109 GGCATGCTGATTTCAAGATTCAAAACATGATG 74
      364 GlnGlnValAsnTyrGluGluPheValGlnMetMet 375

RESULT 9
US-09-554-000-4
; Sequence 4, Application US/09554000
; Patent No. US20020165364A1
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; FILE REFERENCE: 07257/042001
; CURRENT APPLICATION NUMBER: US/09/554,000
; PRIORITY FILING DATE: 2000-04-20
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 652
; TYPE: PR
; ORGANISM: Aequorea victoria
US-09-554-000-4

Alignment Scores:
Pred. No.:      1,596-06      Length:      652
Score:          147.00      Matches:      41
Percent Similarity: 50.66%      Conservative: 36
Best Local Similarity: 26.97%      Mismatches: 57
Query Match:    13.85%      Indels:      18
DB:            10      Gaps:      4

US-10-021-323-13 (1-609) x US-09-554-000-4 (1-652)
Qy      526 GACTTCAACGCGTATTTCGAGAAGCTCGACAAATGAGATGCTTGTATGCTGAG 467
      241 GiuphelyGluAlaPheSerLeuPheAspIleAspGlyThrIleThrArgLys 260
Qy      466 GAGCTGAATGTGCTTCAGAGAAATCGGCTCTGTCCAATTCAGCCTTGAA---GAATTG 410
      261 GluLeuGlyThrValMetArgSerLeuGly-----GlnAsnProThrGlnAlaGluLeu 278
Db      409 GAGCCTTAGTGGGAAACATCTTGAACCTTGAGATTCCTGCTTTATGATTC 350
      279 GlnAspMetIleAsnGluValAspAlaAspGlyAsnGlyThrIleThrArgProGluPhe 298
Qy      349 ATCTGAAACCACTGCGACATGCTGTGACGAAGAGAGAGAGGAATGTGTCATTGAC 290
      299 LeuThrMetMetAlaArgLysMetLysAspThrAspSerGluGluGlu----- 314
Qy      289 GGGCGGCGTGAAGAAGAGACATGACCTTGCGAAGGCTTTTAAGTGTGCTTGAT 230
      315 -----IleArgGluAlaPheArgValPheAspIleAsp 325
Qy      229 GGGATGGTGGGGGAGATGTGAGAGCTTGAATACGTGCTGGAAAGACTGGTATGCA 170
      326 GlnAsnGlyTyrIleSerAlaAlaGluLeuArgHisValMetThrAsnLeuGly----- 343
Qy      169 GGTGAATAATAGTGAAGAAAGACTGCGAGAGCATGATTTGTGATTAACACCAATTGAGAC 110
      344 GluLysLeuThrAspGluGluValAlaAspGluMetIleArgGluAlaAspIleAspGlyAsp 363
Db      109 GGCATGCTGATTTCAAGATTCAAAACATGATG 74
      344 GluLysLeuThrAspGluGluValAlaAspGluMetIleArgGluAlaAspIleAspGlyAsp 363
```

```

QY      109 GGCATGTTGATTTTCAGAAATTCAAAACTGATG 74
      ||| |:::||||| ||| |
Db      364 GlyGlnValAsnTyrGlnGlnPheValGlnMetMet 375

RESULT 10
      US-10-369-493
      ; Sequence 6535, Application US/10369493
      ; Publication No. US2003023675A1
      ; GENERAL INFORMATION:
      ; APPLICANT: Cao, Yongwei
      ; APPLICANT: Hinkle, Gregory J.
      ; APPLICANT: Slater, Steven C.
      ; APPLICANT: Goldman, Barry S.
      ; APPLICANT: Chen, Xianfeng
      ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
      ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
      ; FILE REFERENCE: 38-10 (52052)B
      ; CURRENT APPLICATION NUMBER: US/10/369, 493
      ; CURRENT FILING DATE: 2003-02-28
      ; PRIOR APPLICATION NUMBER: US 60/360, 039
      ; PRIOR FILING DATE: 2002-02-21
      ; NUMBER OF SEQ ID NOS: 4/374
      ; SEQ ID NO 6535
      ; LENGTH: 218
      ; TYPE: PRT
      ; ORGANISM: Caenorhabditis elegans
      US-10-369-493-6535

Alignment Scores:
Pred. No.:      1,26e-06      Length:      218
Score:          146.50      Matches:      42
Percent Similarity: 42.29%      Conservative: 32
Best Local Similarity: 24.00%      Mismatches: 52
Query Match:    13.81%      Indels:      49
Db:             12      Gaps:      4

US-10-021-323-13 (1-609) x US-10-369-493-6535 (1-218)
QY      550 AAAATGTCCTCCCTTGTAGTACGCGACTTGCAACGCGTATCGAAGAGCTGCAAGAT 491
      :::::||||| ::::: ||| |
Db      74 GlnLeuThrProGlnGluIleAspGlnPheArgGluIlePheMetMetPheAspLysAsp 93
      :::::||||| ::::: ||| |
QY      490 GGAGATGCGCTCTTGTAGCTGCGAGAGCTGAATGTTGCTCCAGAGATCGGCTGTGC 431
      ||| |:::||||| ::::: ||| |
Db      94 GlyAsnGlyThrIleSerThrLysGlnLeuGlyIleAlaMetArgSerLeuGlyGlnAsn 113
      :::::||||| ::::: ||| |
QY      430 CAATTGACGCTTGAGAAATGAGACCTTGTAGTGGGAAAAACCATGTTGAACCTTGAGTAA 371
      ||| |:::||||| ::::: ||| |
Db      114 ProThrGlnGlnGlnIleLeuGlnMetIle----- 123
      :::::||||| ::::: ||| |
QY      370 TTCTTGTCTTTTATGATTCATCTCGAACCCACTGGCACATGSGTGGACGAAGAGAG 311
      :::::||||| ::::: ||| |
Db      123 ----- 123
      :::::||||| ::::: ||| |
QY      310 GAGGAGGAATGTGCTCATTCACGCGCGCGGTGAA----- 278
      ||| |:::||||| ::::: ||| |
Db      124 ---AasnGlnValAspIleAspGlyAsnGlyGlnIleGlnPheProGlnPheCysValMet 142
      :::::||||| ::::: ||| |
QY      277 -----GAGAAGACAGTGCACCTTCCGAG--GCTTTAAAGTGT 239
      ||| |:::||||| ::::: ||| |
Db      143 MetLysArgMetMetLysGlnThrAspSerGlnMetIleArgGlnAlaPheArgValPhe 162
      :::::||||| ::::: ||| |
QY      238 GACTTGAATGGGGATGGGTTGGGGGAGATGAGAGAGCTTGAATACGTCGTCGGAAAGACTG 179
      ||| |:::||||| ::::: ||| |
Db      163 AspLysAspGlyAsnGlyValIleIleTrpAlaGlnIlePheArgTyrPheMetValHisMet 182
      :::::||||| ::::: ||| |
QY      178 GGTATGCTGAGTGAATAATAGTGAAGAAAGACTGCGAGACATGATTTGGTATTACAGACC 119
      ||| |:::||||| ::::: ||| |
Db      183 GlyMet-----GlnPheSerGlnGlnValAspIleMetIleLysGlnValAspVal 200
      :::::||||| ::::: ||| |
QY      118 AATTACAGCGCATGGTGTGATTTTCAAGAAATTCAAAAATCATGATG 74
      :::::||||| ::::: ||| |

```

```

Db
201 AspGlyAspGlyGluIleAspPyrGluGluPheValIleAspMetMet 215

RESULT 11
US-09-554-000-6
; Sequence 6, Application US/09554000
; Patent No. US20020165364A1
; GENERAL INFORMATION:
; APPLICANT: TsiEn, Roger Y.
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; FILE REFERENCE: DETECTION OF ANALYTES
; CURRENT APPLICATION NUMBER: 07257/042001
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 08/818,252
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 642
; TYPE: PRT
; ORGANISM: Aequorea victoria

Alignment Scores:
Pred. No.: 3,29e+06 Length: 642
Score: 144.00 Matches: 40
Percent Similarity: 50.66% Conservatave: 37
Best Local Similarity: 26.32% Mismatches: 57
Query Match: 13.57% Indels: 18
DB: 10 Gaps: 4

US-10-021-323-13 (1-609) x US-09-554-000-6 (1-642)
QY 526 GACCTTCAAGCGGTATTCAGAAAGCTCGACAAGATGAGTGCGTTGTTAGCTGGAG 467
Db 241 GlnPheLysGluIleAlaPheSerLeuPheAspGlyAspGlyThrIleThrThrLys 266
QY 466 GAGCTGAATTGCTGCTCCAGAAATCGGGTCTGTCATTCAGCCTTGAA--GAATTG 410
Db 261 GluLeuGlyThrValMetSerIleGly-----GlnAspProThrGluIleGluLeu 278
QY 409 GAGCCTTAGTGGAAAACCATGTTGAACCTTGATGAATCTGTGTTTATGATCC 350
Db 279 GlnAspMetIleAsnGluValAspAlaAspGlyAsnGlyThrIleTyrPheProGluPhe 298
QY 349 ATCTCGAACCCACTGGACATGCTGTGACGAAGAAGAGAGAGAGAGATGTCATTCAC 290
Db 299 LeuThrMetMetAlaArgLysMetLysAspThrAspSerGluGlu----- 314
QY 289 GGGGGGGGTGAAGAAGAACAGTGCAGCTTTCGAAAGCGTTTAAAGTGTGACTGAAT 230
Db 315 -----GCTTTCGAAAGCGTTTAAAGTGTGACTGAAT 230
QY 229 GGGGATGGGTTGGGGGATGTGAGAGCTTGAATACGCTGCTGGAAACATCGGTATGTGA 170
Db 326 GlyAsnGlyTyrIleSerAlaIleGlnLeuArgHisValMetThrAsnLeuGly----- 343
QY 169 GGTGAATAATGAGAAAAGACTGACGACGAGACGTGAATTTGTTACGACACCAATTCAGAC 110
Db 344 GlnLysLeuThrAspGluGluValAspGluMetIleArgGluIleAspIleAspGlyAsp 363
QY 109 GGCATGTTGATTTTCAGAAATTCAAAACATGATG 74
Db 364 GlyGlnValAsnThrGluGluPheValGlnMetMet 375

RESULT 12
US-09-554-000-8
; Sequence 8, Application US/09554000
; Patent No. US20020165364A1
; GENERAL INFORMATION:
; APPLICANT: TsiEn, Roger Y.
; APPLICANT: Miyawaki, Atsushi

```


TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
 TITLE OF INVENTION: DETECTION OF ANALYTES
 FILE REFERENCE: 07257/042001
 CURRENT APPLICATION NUMBER: US/09/554,000
 PRIOR APPLICATION NUMBER: 2000-04-20
 PRIOR FILING DATE: 1997-03-14
 NUMBER OF SEQ ID NOS: 56
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 8
 LENGTH: 656
 TYPE: PRT
 ORGANISM: Aequorea victoria
 US-09-554-000-8

Alignment Scores:
 Pred. No.: 3,31e-06 Length: 656
 Score: 144.00 Matches: 40
 Percent Similarity: 50.66% Conservative: 37
 Best Local Similarity: 26.32% Mismatches: 57
 Query Match: 13.57% Indels: 18
 Gaps: 4

US-10-021-323-13 (1-609) x US-09-554-000-8 (1-656)

QY 526 GACTTGCACGCGTATTCGAGAACTCGAAGATGAGATGCTTCGTTAGTCGAG 467
 DB 257 GluphelygluAlaIpheserleupheaplysaeglyAspGlythrIlethrIys 276
 QY 466 GAGCTGAATGTTGCTCCAGAAATCGGGTCTTCCTCAATTCAGCCTTGA---GAATTG 410
 DB 277 GluleuglyThrValMetarGserleugly-----GlnAsnProthrGluIleu 294
 QY 409 GAGCCCTTGTTGGGAAAACCATGTTGAACCTTGAGATCTCTGCTTTATGATTC 350
 DB 295 GlnAspMetCilaSndluValaSpaIaAspGlyAsnGlyThrIleThrheProGluPhe 314
 QY 349 ATCTGCAACCCACTGGCAGATGATGCTGGTGAAGAGAGAGAGAGATTTGTCATTGAC 290
 DB 315 LeuThrMetMetAlaArglyMetIysAspThrAspSerGluGluIu----- 330
 QY 289 GCGCGCGGTGAAGAAAGACAGTGAACCTTGGCAAGGCTTTAAAGTGTGTAATTGAT 230
 DB 331 -----IleArgGluAlaPheArgValPheAspIysAsp 341
 QY 229 GGGGATGGTGGGGGAGATGAGAGCTTGATAGCTGCTGAGAAAGATGGGTATGTA 170
 DB 342 GlyAsnGlyThrIleSerAlaIaGlnLeuArgHisValMetThrAsnleugly----- 359
 QY 169 GGTGAAAATAGTGAAGAAAGACAGAGATGATGATTTGATTACGACCAATTGACAC 110
 DB 360 GluIysLeuThrAspGluIuValaAspGluMetIleArgGluAlaAspIleAspGlyAsp 379
 QY 109 GGCATGTTGATTTTCAGAAATTCAAAAATCATGATG 74
 DB 380 GlyGlnValaAsnTyrgluGluPheValGlnMetMet 391

RESULT 13
 US-09-988-462-21
 Sequence 21, Application US/09988462
 Publication No. US20030046726A1
 GENERAL INFORMATION:
 APPLICANT: Koziej, Michael G.
 Desai, Nalini M.
 Lewis, Kelly S.
 Kramer, Vance C.
 Warren, Gregory W.
 Evola, Stephen V.
 Crossland, Lyle D.
 Wright, Martha S.
 Merlin, Ellis J.
 Launis, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

INSECTICIDAL ACTIVITY IN MAIZE
 NUMBER OF SEQUENCES: 94
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Syngenta Biotechnology, Inc.
 STREET: 3054 Cornwallis Road
 CITY: Research Triangle Park
 STATE: NC
 COUNTRY: USA
 ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/988,462
 FILING DATE: 20-NOV-2003
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/547,422
 FILING DATE: 11-APR-2000
 APPLICATION NUMBER: US 08/459,504
 FILING DATE: 02-JUN-1995
 APPLICATION NUMBER: US 07/951,715
 FILING DATE: 25-SEP-1992
 APPLICATION NUMBER: US 07/772,027
 FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Weig, J. Timothy
 REGISTRATION NUMBER: 38,241
 REFERENCE/DOCKET NUMBER: S-188051
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919)541-8587
 TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 408 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 21:

US-09-988-462-21

Alignment Scores:

Pred. No.: 3.63e-06 Length: 408
 Score: 143.00 Matches: 45
 Percent Similarity: 44.97% Conservative: 31
 Best Local Similarity: 26.63% Mismatches: 63
 Query Match: 13.48% Indels: 30
 Gaps: 4

US-10-021-323-13 (1-609) x US-09-988-462-21 (1-408)

QY 562 CTCCTTGGTGAATATGTCCTCCCTTAGTAAAGCCGATTCGAGAG 503
 DB 244 IleIleIaGlyCylseSerGluIuIleThrGlyLeuIysGluMetheIysAsn 263
 QY 502 CTCGACAAAGATGAGATGCGCTTGTAGTCTGAGAGAGCTGAATTGCTGTCAGACA 443
 DB 264 IleAspIysAspAsnSerGlyThrIleThrIleuAspGluIleuIysGlyLeuAlaIys 283
 QY 442 ATCGGCTGTGCAATTCAGCCTTGAAGAAATTCGAGCCCTTAGTG----- 398
 DB 284 HisGlyPro--LysLeuSerAspSerGluMetGluIysLeuMetGluAlaIaAspAla 302
 QY 397 ---GGAAAACCATGTTGAATTCGATGATGATTTCTTTATGATTCATTCGAC 341
 DB 303 AspGlyAsnGlyLeuIleAspIysAspGluPheVal----- 314
 QY 340 CCATCGGACATGCTGTCGACAAAGAGAGAGAGAGATTTGTCATTTCAGCGCGCGGT 281
 DB 315 -----ThrAlaThrValHisMetAsnIys 322

QY 280 GAAGAAGACAGTGCCTTGCAGAGCTTTTAAAGTTGACTTGAATGGGATGG 221
: : : : :
: : : : :
Db 323 LeuAspArgGluGlnHisLeuTyrThrAlaPheGlnTyrPheAspIysAspSerGly 342
: : : : :
QY 220 TTGGGGGGATGTGAGAGCTTGAATACGTCGCGAAGCTGGTATGAGCTGAAT 161
: : : : :
Db 343 TyrIleThrLysGluGlnLeuGlnHisAlaLeuLysGluGlnGlyLeuTyrAspAlaAsp 362
: : : : :
QY 160 AGTGAAGAAAGATCGACGACATGATTTGTTATTCAGACCAATTACAGCGCATGTT 101
: : : : :
Db 363 LysIleLysAsp-----IleIleSerAspAlaAspSerAspAsnAspIlyArgIle 379
: : : : :
QY 100 GATTTTCAAGAAATTCAAAAACATGATG 74
: : : : :
Db 380 AspTyrSerGluPheValAlaMetMet 388
: : : : :
RESULT 14
US-09-988-462-22
; Sequence 22, Application US/09988462
; Publication No. US20030046726A1
; GENERAL INFORMATION:
; APPLICANT: Kozziel, Michael G.
; Deas, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Launis, Karen L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Syngenta Biotechnology, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/988,462
; FILING DATE: 20-NO. US20030046726A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/547,422
; FILING DATE: 11-APR-2000
; APPLICATION NUMBER: US 08/459,504
; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-188051
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8687
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 464 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..464
; OTHER INFORMATION: /note= "derived protein sequence of
; pollen specific CDPK as disclosed in Figure 34."
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-988-462-22
Alignment Scores:
Pred. No.: 3,79e-06 Length: 464
Score: 143.00 Matches: 45
Percent Similarity: 44.97% Conservative: 31
Best Local Similarity: 26.63% Mismatches: 63
Query Match: 13.48% Indels: 30
DB: 11 Gaps: 4
US-10-021-323-13 (1-609) x US-09-988-462-22 (1-464)
QY 562 CTCCTTGTGTGTAATAATGCCCCCTTAGTAAGACCGACTTGAACCGCTATTCGAGAAG 503
: : : : :
Db 306 IleIleIleGlyCysLeuSerGluGlnGluIleThrGlyLeuLysGluMetPheLysAsn 325
: : : : :
QY 502 CTCGACAAAGATGAGATGCTTGTGTTAGTGTGAGAGCTGAAATGGTCTCCAGAGA 443
: : : : :
Db 326 IleAspLysAspAsnSerGlyThrIleThrLeuAspGluLeuLysHisGlyLeuAlaLys 345
: : : : :
QY 442 ATCGGCTCTGCCAATTCAGCCTTGAAGAAATTCAGACCCCTTAGG----- 398
: : : : :
Db 346 HisGlyPro--LysLeuSerAspSerGluMetGluLysLeuMetGluAlaAlaAspAla 364
: : : : :
QY 397 ---GAAAAACCATTTGAACTTGAGATGAAATCTTGTCTTTTATGAAATCCATCTCGAAC 341
: : : : :
Db 365 AspGlyAsnGlyLeuIleAspTyrAspGluPheVal----- 376
: : : : :
QY 340 CCACTGGCACAATGTTGTGACGAAGAAGAGAGAGAAATTCATTCACGCGGCGCT 281
: : : : :
Db 377 -----ThralaThrValHisMetAsnLys 384
: : : : :
QY 280 GAAGAAGACAGTGCCTTGCAGAGCTTTTAAAGCTTGAATGAGGATGGGATGG 221
: : : : :
Db 385 LeuAspArgGluGlnHisLeuTyrThrAlaPheGlnTyrPheAspLysAspAsnSerGly 404
: : : : :
QY 220 TTGGGGGGATGTGAGAGCTTGAATACGTCGCGAAGCTGGTATGAGCTGAAT 161
: : : : :
Db 405 TyrIleThrLysGluGlnLeuGlnHisAlaLeuLysGluGlnGlyLeuTyrAspAlaAsp 424
: : : : :
QY 160 AGTGAAGAAAGATCGACGACATGATTTGTTATTCAGACCAATTACAGCGCATGTT 101
: : : : :
Db 425 LysIleLysAsp-----IleIleSerAspAlaAspSerAspAsnAspIlyArgIle 441
: : : : :
QY 100 GATTTTCAAGAAATTCAAAAACATGATG 74
: : : : :
Db 442 AspTyrSerGluPheValAlaMetMet 450
: : : : :
RESULT 15.
US-10-369-493-6260
; Sequence 6260, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 6260
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6260

Alignment Scores:

Pred. No.:	3.35e-06	Length:	149
Score:	142.00	Matches:	42
Percent Similarity:	48.10%	Conservative:	34
Best Local Similarity:	26.58%	Mismatches:	52
Query Match:	13.38%	Indels:	30
DB:	12	Gaps:	6

US-10-021-323-13 (1-609) x US-10-369-493-6260 (1-149)

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QY      526 GACTTGCAACGCGTATTCCAGAAAGCTCGACAGAAATGAGATGCTTCCTTACTCTGGAG 467
      :::::
DB      12 GIupheLygLuAlaPheSerLeuPheAspLyAspGlyThrIleThrThryS 31
      :::::
QY      466 GAGCTGAATGGTGTCTCCAGAGAAATCGGAGTGTCCCAATTGACCTTGAA---GAATTG 410
      |||||
DB      32 GIuLeuGlyThrValMetArgSerLeuGly-----GIhAsnProThrGIuAlaGIuLeu 49
      :::::
QY      409 GAGCCCTTAAGT-----GGAAACCATGTTTGAACCTTGATGAATTC 368
      :::::
DB      50 GIAspMetIleAsnGIuValAspAlaAspGlyAsnGlyThrIleAspPheProGIuPhe 69
      :::::
QY      367 TTGTTCTTTTATGATTCATCTCGAACCACTGGCACATGCTGTGTGACGAAAGAGAGAG 308
      |||
DB      70 Leu-----ThMetMetAlaArgLyseMetLyAspThrAspSer 82
      :::::
QY      307 GAGGAATTGGTCAATTCACGCGCGCGGTGAAGAAAGACAGACAGTGCCTTGCAGAGCTTTT 248
      |||||
DB      83 GIuGIu-----GIuIleArgGIuAlaPhe 90
      :::::
QY      247 AAAGTGTTCAGTTCGATGCGGATGGGATGGGCGGATGTGAGGAGCTTGAAATACGTGCTG 188
      :::::
DB      91 ArgValPheAspLyAspGIyAsnGlyPheIleSerAlaIaGIuLeuArgHisValMet 110
      :::::
QY      187 GGAAGACTGGGTATGTGAGGTGAAAAATAGTGAAGAAAGACTGCAGAGCATGATTGGTAT 128
      |||||
DB      111 ThrAsnLeuGly-----GIuLySLeuThrAspGIuGIuValAspGIuMetIleArgGIu 128
      :::::
QY      127 TCGACACCAATTCAGACGCGCATGCTTGATTTTCAAGAAATTCAAAAACATGATG 74
      |||||
DB      129 AlaAspIleAspGIyAspGIyGIuValAsnTyGIuGIuPheValThrMetMet 146
      :::::
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Search completed: January 31, 2004, 02:46:06
Job time : 50.5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 31, 2004, 00:30:10 ; Search time 61 Seconds
(without alignments)
4406.596 Million cell updates/sec

Title: US-10-021-323-13

Perfect score: 609

Sequence: 1 ggaatgaatcaacattt.....tgaagcttacaattaag 609

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA: *
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/2/ina/ECTUS_COMB.seq: *
6: /cgn2_6/ptodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51.6	8.5	7218	1	US-08-232-463-14
2	40	6.6	1052	1	US-08-466-603-1
3	40	6.6	1052	1	US-08-314-503A-1
4	40	6.6	1052	1	US-08-466-066-1
5	40	6.6	1052	2	US-08-466-717-1
6	40	6.6	1052	3	US-08-466-743-1
7	40	6.6	1052	5	PCT-US95-12414-1
8	39.8	6.5	289	3	US-09-007-005-17
9	39.8	6.5	289	3	US-09-244-796-17
10	37.8	6.2	966	2	US-08-766-738-2
11	37.8	6.2	966	4	US-09-262-610-2
12	36.2	5.9	1965	3	US-09-178-252-26
13	35.6	5.8	3211	2	US-08-574-959A-8
14	35.6	5.8	3211	3	US-09-357-014-8
15	35.6	5.8	3207	2	US-08-574-959A-6
16	35.6	5.8	3207	3	US-09-357-014-6
17	35.4	5.8	3489	2	US-08-728-323A-1
18	35.4	5.8	3489	4	US-09-298-568-1
19	35.4	5.8	3489	4	US-09-410-399-1
20	35.4	5.8	32207	2	US-08-770-379-20
21	35.4	5.8	32207	3	US-08-757-669A-20
22	35.4	5.8	32207	4	US-09-230-371A-20
23	34.4	5.6	856	4	US-09-171-517B-15
24	34.4	5.6	4161	4	US-09-185-244-8
25	34.4	5.6	4161	4	US-09-471-913-1
26	34.4	5.6	12241	4	US-09-948-138-4
27	34.4	5.6	13737	4	US-09-538-414-10

28	33.6	5.5	2082	3	US-09-440-325A-2	Sequence 2, Appl1
29	33.6	5.5	2082	4	US-09-846-996A-2	Sequence 2, Appl1
30	33.6	5.5	7183	4	US-09-081-149-9	Sequence 9, Appl1
31	33.6	5.5	7183	4	US-09-081-149-10	Sequence 10, Appl1
32	33.4	5.5	2277	1	US-08-676-967-2	Sequence 2, Appl1
33	33.4	5.5	2277	1	US-08-676-967-2	Sequence 2, Appl1
34	33.4	5.5	2277	2	US-09-098-487-2	Sequence 2, Appl1
35	33.2	5.5	3624	2	US-07-951-715A-6	Sequence 6, Appl1
36	33.2	5.5	3624	2	US-08-459-448A-6	Sequence 6, Appl1
37	33.2	5.5	3624	3	US-08-459-448A-6	Sequence 6, Appl1
38	33.2	5.5	3624	3	US-08-459-448A-6	Sequence 6, Appl1
39	33.2	5.5	3624	3	US-08-459-448A-6	Sequence 6, Appl1
40	33.2	5.5	3624	3	US-09-053-549-7	Sequence 7, Appl1
41	33.2	5.5	3624	4	US-09-547-422-6	Sequence 6, Appl1
42	33.2	5.5	7001	1	US-08-258-261B-1	Sequence 1, Appl1
43	33.2	5.5	7001	1	US-08-456-837-1	Sequence 1, Appl1
44	33.2	5.5	7001	1	US-08-457-342-1	Sequence 1, Appl1
45	33.2	5.5	7001	1	US-08-457-646A-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-08-232-463-14
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHRIFFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZpTc-F18
US-08-232-463-14
Query Match 8.5%; Score 51.6; DB 1; Length 7218;

Best Local Similarity 3.8%; Pred. No. 1.2e-05;
Matches 15; Conservative 221; Mismatches 160; Indels 0; Gaps 0;

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QY 140 GGTCTGAGTCTTTTCCATTTTCACTACATACCCAGCTCTCCAGACGATATTC 199
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Db 1058 GCTTGCATATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1117
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QY 200 AAGTCTCATACCCGCCCAACCATCCCATTAAGTCAAAACATTAAAGCTTGGC 259
    : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1118 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1177
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QY 260 AAGTCACTGCTCTTCTTCAACGCGCGCGTAATGACCAATTCCTCTCTCTTC 319
    : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1178 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1237
    : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 320 GTCACACACATGCGCAGTGGGTGAGATGATTCATTAAGAAACAAATTCATCCA 379
    : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1238 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1297
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QY 380 GTTCAAAACATGTTTTCCACTAAGGCTCAATTCCTCAAGCTGAATGACAGACCC 439
    : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1298 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1357
    : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 440 GATCTCTGAGCAACCAATTCAGCTCTCTCAGACTAAGCAAGCATCTCATCTGTC 499
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Db 1358 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1417
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QY 500 GAGCTTCTGATAGCGCTTGAAGTCTTACT 535
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Db 1418 YYYYYYYYYYYYYYGTACCAATTTCTTATCT 1453
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RESULT 2

US-08-466-603-1/c

Sequence 1, Application US/08466603
Patent No. 5726018
GENERAL INFORMATION:
APPLICANT: Pasternack, Gary R.
APPLICANT: Kuhnajda, Francis P.
TITLE OF INVENTION: No. 5726018el Mammalian Protein Associated With
TITLE OF INVENTION: Uncontrolled Cell Division
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,603
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,503
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Posorske Esq., Laurence H.
REGISTRATION NUMBER: 34,698
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9299
TELEFAX: 202 508-9153
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1052 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 97..843
US-08-466-603-1

Query Match 6.6%; Score 40; DB 1; Length 1052;
Best Local Similarity 46.7%; Pred. No. 0.017;
Matches 127; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

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QY 59 AGAAGGAGATGATACATCATGTTTGAATTTGAAATCAACATGCGGTGAAT 118
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 879 ACAATAGAAATTTTCAAAATAGATATTCATTCATGATCATCTTCTCTATCTTC 820
    : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 119 GGTGTGTAATACCAATGATGCTCTGCACTTTTTCAGTATTTTCACTCATAC 178
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 819 AGTTCTGTTTGGCTTCTGACCCCTTCTTTCACAGCTCTTCTCATCTTCTCTC 760
    : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 179 CAGTCTCCAGACGATTTAAGTCTCTCAATCCCCCAACCATCCCATTCAGTC 238
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 759 GTCATCTACCTCTCATCGTTATTAACCTTTTCATCTCTCTCTCTCTCTCACTG 700
    : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 239 AAACATTTAAAGCTTTCGCAAGTCACTGCTCTTCTTCTTCAACGCGCGGTGAATGAC 298
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 699 CTCCTTTCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 640
    : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 299 CAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 330
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 639 TTCAATCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 608
    : : : : : : : : : : : : : : : : : : : : : : : : : :
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RESULT 3

US-08-314-503A-1/c

Sequence 1, Application US/08314503A
Patent No. 5734022
GENERAL INFORMATION:
APPLICANT: Pasternack, Gary R.
APPLICANT: Kuhnajda, Francis P.
TITLE OF INVENTION: No. 5734022el Mammalian Protein Associated With
TITLE OF INVENTION: Uncontrolled Cell Division
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/314,503A
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Posorske Esq., Laurence H.
REGISTRATION NUMBER: 34,698
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9299
TELEFAX: 202 508-9153
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1052 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 97..843
US-08-314-503A-1

Query Match 6.6%; Score 40; DB 1; Length 1052;
Best Local Similarity 46.7%; Pred. No. 0.017;
Matches 127; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

QY 59 AGAAGGGAATGTAATCATCATGTTTGAATCTTGAATAACACATCCGCTGAATT 118
DB ACAATAGGAATTTTCAAAATAGTTATTCAGTATCATCATCTTCCCTCATCTTC 820
QY 119 GGTGCTGAATACCAATCATGCTCTGAGTCTTTTCCATATTTCACCTACATACC 178
DB 819 AGTTCTGTTTCCCTCTGACCCCTTCTTCCACCAAGCTCTTTCATCTTCCCTC 760
QY 179 CAGTCTCCAGCAGATGATTCAGCTCCACATCCCGCAACGATCCCATTCAGATC 238
DB 759 GTCATCTACCTCTCATGTTAATCACTTTCATCTCTCTCTCTCTCTCTCTCTCT 700
QY 239 AAACACTTAAAGCCTTCGCAAGGTCACTGCTTCTTCTTCCACGCGCGCTGAATAC 298
DB 699 CTCCTCTACCT 640
QY 299 CAATCT 330
DB 639 TTCATCATCT 608

RESULT 4

US-08-468-066-1/c
Sequence 1, Application US/08468066
Patent No. 5756676

GENERAL INFORMATION:
APPLICANT: Pasternack, Gary R.
TITLE OF INVENTION: No. 5756676e1 Mammalian Protein Associated With
TITLE OF INVENTION: Uncontrolled Cell Division
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,066
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,503
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Posorske Esq., Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107.47218
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9153
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1052 base pairs
TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 97..843
US-08-468-066-1

Query Match 6.6%; Score 40; DB 1; Length 1052;
Best Local Similarity 46.7%; Pred. No. 0.017;
Matches 127; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

QY 59 AGAAGGGAATGTAATCATCATGTTTGAATCTTGAATAACACATCCGCTGAATT 118
DB 879 ACAATAGGAATTTTCAAAATAGTTATTCAGTATCATCATCTTCCCTCATCTTC 820
QY 119 GGTGCTGAATACCAATCATGCTCTGAGTCTTTTCCATATTTCACCTACATACC 178
DB 819 AGTTCTGTTTCCCTCTGACCCCTTCTTCCACCAAGCTCTTTCATCTTCCCTC 760
QY 179 CAGTCTCCAGCAGATGATTCAGCTCCACATCCCGCAACGATCCCATTCAGATC 238
DB 759 GTCATCTACCTCTCATGTTAATCACTTTCATCTCTCTCTCTCTCTCTCTCTCT 700
QY 239 AAACACTTAAAGCCTTCGCAAGGTCACTGCTTCTTCTTCCACGCGCGCTGAATAC 298
DB 699 CTCCTCTACCT 640
QY 299 CAATCT 330
DB 639 TTCATCATCT 608

RESULT 5

US-08-466-717-1/c
Sequence 1, Application US/08466717
Patent No. 5874234

GENERAL INFORMATION:
APPLICANT: Pasternack, Gary R.
TITLE OF INVENTION: No. 5874234e1 Mammalian Protein Associated With
TITLE OF INVENTION: Uncontrolled Cell Division
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,717
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,503
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Posorske Esq., Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107.47218
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9153
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 1052 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE: CDNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 97..843
US-08-466-717-1

Query Match 6.6%; Score 40; DB 2; Length 1052;
Best Local Similarity 46.7%; Pred. No. 0.017;
Matches 127; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

QY 59 AGAAGGGAATGTAATCATCATCTTTTGAATTTGAAATACACATGCCGTGAATT 118
DB 879 ACAATAGGAATTTTCAAAATAGTTATTCACCTAGTCATCATCTTCCCTCATCTTC 820
QY 119 GGTGTGTAATACCAATCATGCTCTGCACTTTTCCACTATTTTCACTCACAATACC 178
DB 819 AGTTCTGTGTTTCCCTTCTGACCCCTTTTCTTTCACCAAGCTTTTTCATCTTCTC 760
QY 179 CAGTCTCCGACGAGTAATCAAGCTCTCACATCCCCCAACCCATCCCATTAAGTC 238
DB 759 GTCATCTACCTCTCATGCTTATTAACCTTTCATCTCTCTCTCCCTGCACTCAGTC 700
QY 239 AAACCTTTAAAGCTTTCGCAAGTCACTGTTCTTTTACGCGCGCGGTGAATGAC 298
DB 699 CTCCTCTTACCTTCT 640
QY 299 CAATTCCT 330
DB 639 TTCATCATCT 608

RESULT 6

US-08-466-743-1/c
Sequence 1, Application US/08466743

Patent No. 6040173
GENERAL INFORMATION:
APPLICANT: Pasternack, Gary R.
APPLICANT: Kuhlaida, Francis P.
TITLE OF INVENTION: No. 6040173el Mammalian Protein Associated With
TITLE OF INVENTION: Uncontrolled Cell Division
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,743
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/314,503
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Posorske Esq., Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107.47218
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9153
TELEFAX: 202 508-9299

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1052 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE: CDNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 97..843
US-08-466-743-1

Query Match 6.6%; Score 40; DB 3; Length 1052;
Best Local Similarity 46.7%; Pred. No. 0.017;
Matches 127; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

QY 59 AGAAGGGAATGTAATCATCATGTTTGAATTTGAAATCAACATGCCGTGAATT 118
DB 879 ACAATAGGAATTTTCAAAATAGTTATTCACCTAGTCATCATCTTCCCTCATCTTC 820
QY 119 GGTGTGTAATACCAATCATGCTCTGCACTTTTCCACTATTTTCACTCACAATACC 178
DB 819 AGTTCTGTGTTTCCCTTCTGACCCCTTTTCTTTCACCAAGCTTTTTCATCTTCTC 760
QY 179 CAGTCTCCGACGAGTAATCAAGCTCTCACATCCCCCAACCCATCCCATTAAGTC 238
DB 759 GTCATCTACCTCTCATGCTTATTAACCTTTCATCTCTCTCTCTCCCTGCACTCAGTC 700
QY 239 AAACCTTTAAAGCTTTCGCAAGTCACTGTTCTTTTACGCGCGCGGTGAATGAC 298
DB 699 CTCCTCTTACCTTCT 640
QY 299 CAATTCCT 330
DB 639 TTCATCATCT 608

RESULT 7

PCT-US95-12414-1/c
Sequence 1, Application PC/TUS9512414

GENERAL INFORMATION:
APPLICANT: Pasternack, Gary R.
APPLICANT: Kuhlaida, Francis P.
TITLE OF INVENTION: Novel Mammalian Protein Associated With
TITLE OF INVENTION: Uncontrolled Cell Division
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/12414
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,503
FILING DATE: 22-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hoscheit Esq., Dale H.
REGISTRATION NUMBER: 19,090
REFERENCE/DOCKET NUMBER: 1107.51507
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9153

TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1052 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 97..843
PCT-US95-12414-1

Query Match 6.6%; Score 40; DB 5; Length 1052;
Best Local Similarity 46.7%; Pred. No. 0.017;
Matches 127; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

QY 59 AGAAGCGAATGTAACATCATGTTTGAATCTTGAATCAACCATGCGTGAATT 118
DB 879 ACAAATGGAATTTTCAAAATAGTTATTCACCTAGTATCATCTTCCCTCATCTTC 820
QY 119 GGTCGTGAATACCAATCATGCTCTGAGTCTTTTCCACTATTTTCACTCATAC 178
DB 819 AGGTCCTCGTTTCCGCTCTGACCCCTTCTTTCACCAAGCTCTTCACTCTTC 760
QY 179 CAGCTTCCAGAGCATTAACAGTCTCCACATCCCCCAACCCATCCCAATGAAGTC 238
DB 759 GTCACTACCTCTCCATCGTTTAACTTCTTCACTCTCTCTCTCTCTCACTAC 700
QY 239 AAACACTTTAAAGCCTTGCAAGTCACTGTTCTTCTTCTTCAACGCGCCGGAATGAC 298
DB 699 CTCCTCTTACCT 640
QY 299 CAATCT 330
DB 639 TTCATCATCT 608

RESULT 8
US-09-007-005-17/c

Sequence 17, Application US/09007005B
Patent No. 6258558
GENERAL INFORMATION:
APPLICANT: Szostak, Jack W.
APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Rihc
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
FILE REFERENCE: 00786/350003
CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT FILING DATE: 1998-01-14
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 289
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Translation template
NAME/KEY: misc_feature
LOCATION: (1)...(289)
OTHER INFORMATION: n = A,T,C or G
US-09-007-005-17

Query Match 6.5%; Score 39.8; DB 3; Length 289;
Best Local Similarity 8.2%; Pred. No. 0.011;

Matches 20; Conservative 102; Mismatches 123; Indels 0; Gaps 0;
QY 157 CACTATTTACCTACATACCAAGTCTTCCAGACGATTAACAGTCTTCAATCCC 216
DB 245 YAGGTTTAACTGCTAAGCTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 186
QY 217 CCAACCCATCCCATTAAGTCAAAACCTTAAAGCTTGCAAGTCACTGCTCTT 276
DB 185 YNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNN 126
QY 277 CTTACCGCCCGCGGATGACCAATTCCTCTCTCTCTCTCTCTCTCTCTCTCT 336
DB 125 YNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNN 66
QY 337 GTGGGTTGAGATGATCATTAAGAACAAATTCATCAAGTCAAGTCAAGTCTTC 396
DB 65 YNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNN 6
QY 397 CCACT 401
DB 5 YCYCY 1

RESULT 9
US-09-244-796-17/c

Sequence 17, Application US/09244796
Patent No. 6281344
GENERAL INFORMATION:
APPLICANT: Szostak, Jack W.
APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Rihc
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
FILE REFERENCE: 00786/350007
CURRENT APPLICATION NUMBER: US/09/244,796
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 289
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Translation template
NAME/KEY: misc_feature
LOCATION: (1)...(289)
OTHER INFORMATION: n = A,T,C or G
US-09-244-796-17

Query Match 6.5%; Score 39.8; DB 3; Length 289;
Best Local Similarity 8.2%; Pred. No. 0.011;
Matches 20; Conservative 102; Mismatches 123; Indels 0; Gaps 0;

QY 157 CACTATTTACCTACATACCAAGTCTTCCAGACGATTAACAGTCTTCAATCCC 216
DB 245 YAGGTTTAACTGCTAAGCTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTG 186
QY 217 CCAACCCATCCCATTAAGTCAAAACCTTAAAGCTTGCAAGTCACTGCTCTT 276
DB 185 YNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNN 126
QY 277 CTTACCGCCCGCGGATGACCAATTCCTCTCTCTCTCTCTCTCTCTCTCTCT 336
DB 125 YNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNN 66
QY 337 GTGGGTTGAGATGATCATTAAGAACAAATTCATCAAGTCAAGTCAAGTCTTC 396


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: CURRENT APPLICATION NUMBER: US/09/178,252
: CURRENT FILING DATE: 1998-10-23
: EARLIER APPLICATION NUMBER: 60/065,215
: EARLIER FILING DATE: 1997-11-12
: EARLIER APPLICATION NUMBER: 60/076,445
: EARLIER FILING DATE: 1998-03-02
: NUMBER OF SEQ ID NOS: 27
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 26
: LENGTH: 1965
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetic B.t. toxin gene
US-09-178-252-26

```

Query Match	5.9%	Score 36.2	DB 3	Length 165
Best Local Similarity	52.3%	Pred. No. 0.34		
Matches 80	Conservative	0	Mismatches 73	Indels 0
				Gaps 0

Qy	176	ACCGAGTTCCTCCGACGAGTATTCAGCTCTCCACATCCCCCAACCATCCCCATTCAA	235
Db	1336	ACCAACGCCGCGCAACCTGCGCACGAGACCTCACACACCGAGAGCTCCCCGTGAG	1395
Qy	236	GTCAAAAGCTTTAAAAGCTTCGCAAGTGCACCTGCTCTTTCAACGCCGCGGTGAT	295
Db	1396	AACAAACAATTCAACCTCTCTCTCCACAGTACCTTCTCTCGCTTAAACACCAACCAAGGC	1455
Qy	296	GACCAATTCTCTCTCTCTCTCTTGTGTACACAC	328
Db	1456	GGCCCACTCGACAGCTGGGGTCTCTCCGACC	1488

RESULT 13
US-08-574-959A-8/c
Sequence 8, Application US/08574959A
Patent No. 5963324

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;	NAME/KEY:	CDS
;	LOCATION:	439..3157
US-08-574-959A-8		

Query Match	5.8%	Score 35.6;	DB 2;	Length 321;
Best Local Similarity	49.5%;	Pred. NO. 0.65;		
Matches 92;	Conservative 0;	Mismatches 94;	Indels 0;	Gaps 0;

QY	150	TCCTTTCCACGATTTTACCCGACATPCCAGCTTCCACAGATTTCAAGCTCCCA	209
Db	2609	TCCTCTTCTCTTCTTCTCTTACTACCTTCTTCTCTCAAAATCTTCTCTCAAACTCT	2556
QY	210	CATCCCCCAACCCATGCCCATTCGATCAAGTCAAACTTTAAAGCCTTGGCAAGTCACTG	269
Db	2549	TCCTTCCTCCTCTTCTCTCTCTTCAAAAATATCTCTTCAATCTCTTCTCTTCTCTCAAAAG	2496
QY	270	TCCTTCTTCTTACCGCGCGCGGTGAATAGCAATTCCTCTCTCTCTTGTGTCACACCA	329
Db	2489	TCCTTCCCTCCTTCT	2430
QY	330	TGTGCGC	335
Db	2429	TCCTTCC	2424

RESULT 14
US-09-357-014-8/c
: Sequence 8, Application US/09357014

GENERAL INFORMATION:

APPLICANT: Jaekyoon Shin, Insil Jung, Ratna K. Vadlamudi

;; TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
; AND USES THEREFOR

CORRESPONDENCE ADDRESS:

STREET: 60 State Street, Suite 510
CITY: Boston

STATE: Massachusetts
COUNTRY: USA

ZIP: 02109-1875
COMPTON READABLE EOBM:

COMPUTER: IBM PC compatible

```
PC-DOS/MS-DOS  
OPERATING SYSTEM:  
SOFTWARE: Patent In Release #1.0 Version #1.25
```

APPLICATION NUMBER: US/09/357.014

LEADS DATA: 10-04-1999
PRIOR APPLICATION DATA:

FILING DATE: <Unknown>

NAME: Mandragouras, Amy E

REFERENCE/DOCKET NUMBER: DFN-008

TELEPHONE: (617) 227-7400

INFORMATION FOR SEQ ID NO: 8:

LENGTH: 3211 base pairs
TYPE: nucleic acid

STRANDEDNESS: Single
TOPOLOGY: Linear

MODECODE TYPE: CDNA
FEATURE:

LOCATION: 439..3157

US-09-357-014-8

US-09-357-014-8

Db 489 GATCATCTTCTCACTCTCTCCATTTCTCCACCTTACAGGTAACCAAGTTTCTTGAGAAC 430
Qy 194 GATTCAGAGCTCTCATACATCCCAACCAATCCCATTCAGTCAAAACATTAAAGC 253
Db 429 AGTTTGAGGTTCTTAGCGGAGATGATCATCATCCGTTCTCATCAACCTTAAAGCC 370
Qy 254 CTTCGCAAGGTCATGTCTTCTTCTTCAACCGCGCCGTAATGACCAATTCCTCTCTCTC 313
Db 369 CTTCGCGAGATC---CGATTCAATTTTCACTGCGGAAAGAGATCATCTTCGTTTCTCC 313
Qy 314 CTCTTGTCACCAACATGTGCCAGTGGGTTGAGATGATTCATTAAGAACAAAGAAATTC 373
Db 312 TCCTCCACAGCTCCACCGAAGAAATGTCAGTGTGTTGTGTAAGAGAAAGAAATTC 253
Qy 374 ATCCAGTTCAAAACATGTTTCCCACTAAGGCTCCAAATTC 415
Db 252 ATCGAAATTTGAGACCAAGTGTACAGGTTGATGTATGATTC 211

RESULT 5

US-09-938-842A-2017/c
; Sequence 2017, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2017
; LENGTH: 576
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2017

Query Match 9.1%; Score 55.6; DB 12; Length 576;
Best Local Similarity 49.7%; Pred. No. 1e-06;
Matches 170; Conservative 0; Mismatches 169; Indels 3; Gaps 1;

Qy 74 CATCATGTTTGAATTTCTTAATAATCAACATCCGCTGTAATGGTGTCTAATACCA 133
Db 549 CATCATGTTTGAATTTCTTAATAATAAGTCAACGCAACCATCTGATCCGTTCAACGGAAC 490
Qy 134 AATCATGCTCCGAGCTCTTTTCCATATTTTCACTCACTCAATACCAAGCTTCCAGCAGC 193
Db 489 GATCATCTTCTCACTCTCTCCATTTTTCACCTTGAAGTAAACCAAGTTTCTTGAGAAC 430
Qy 194 GATTCAGAGCTCTCATACATCCCAACCAATCCCATTCAGTCAAAACATTAAAGC 253
Db 429 AGTTTGAGGTTCTTAGCGGAGATGATCATCATCCGTTCTCATCAACCTTAAAGCC 370
Qy 254 CTTCGCAAGGTCATGTCTTCTTCTTCAACCGCGCCGTAATGACCAATTCCTCTCTCTC 313
Db 369 CTTCGCGAGATC---CGATTCAATTTTCACTGCGGAAAGAGATCATCTTCGTTTCTCC 313
Qy 314 CTCTTGTCACCAACATGTGCCAGTGGGTTGAGATGATTCATTAAGAACAAAGAAATTC 373
Db 312 TCCTCCACAGCTCCACCGAAGAAATGTCAGTGTGTTGTGTAAGAGAAAGAAATTC 253
Qy 374 ATCCAGTTCAAAACATGTTTCCCACTAAGGCTCCAAATTC 415
Db 252 ATCGAAATTTGAGACCAAGTGTACAGGTTGATGTATGATTC 211

Db 252 ATCGAAATTTGAGACCAAGTGTACAGGTTGATGTATGATTC 211

RESULT 6

US-09-938-842A-1697/c
; Sequence 1697, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1697
; LENGTH: 510
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1697

Query Match 8.8%; Score 53.6; DB 10; Length 510;
Best Local Similarity 52.7%; Pred. No. 4e-06;
Matches 116; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

Qy 74 CATCATGTTTGAATTTCTTAATAATCAACATCCGCTGTAATGGTGTCTAATACCA 133
Db 480 CATCATGTAAGAAACTCTTGTATGATGATCTACATCACCATCTGCATCAACTTGAT 421
Qy 134 AATCATGCTCCGAGCTCTTTTCCATATTTTCACTCACTCAATACCAAGCTTCCAGCAGC 193
Db 420 AATCATCTTCTTACCAACATCTAGGGTCTTCCCTGTGAGTCCCAAGAGCCATAC 361
Qy 194 GATTCAGAGCTCTCATACATCCCAACCAATCCCATTCAGTCAAAACATTAAAGC 253
Db 360 AGATTTCAGCTCTTCAAGAGATGATTAACCATCTCCGTTGGTCAACAGTTAAAGC 301
Qy 254 CTTCGCAAGGTCATGTCTTCTTCTTCAACCGCGCCGCTGA 293
Db 300 ATCTTCATATCTCTCTCTCTGTTTCCGCAATCGTTGTA 261

RESULT 7

US-09-938-842A-1697/c
; Sequence 1697, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1697

;; CURRENT APPLICATION NUMBER: US/10/273,334
;; CURRENT FILING DATE: 2002-10-18
;; PRIOR APPLICATION NUMBER: US/09/591,500
;; PRIOR FILING DATE: 2000-12-06
;; PRIOR APPLICATION NUMBER: PCT/US98/26433
;; PRIOR FILING DATE: 1998-12-11
;; PRIOR APPLICATION NUMBER: US 60/069,677
;; PRIOR FILING DATE: 1997-12-11
;; NUMBER OF SEQ ID NOS: 51
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 19
;; LENGTH: 905
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (64)..(453)
;; OTHER INFORMATION:
US-10-273-334-19

Query Match 7.1%; Score 43; DB 16; Length 905;
Best Local Similarity 47.0%; Pred. No. 0.013;
Matches 133; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

QY 48 AGAATACTCAAGAAAGGGAATGTAAACATCATGTTTGAATTTGAAATCAACCATG 107
DB 857 ACAGTAAATACAAAAGAAATTTTCAAAATAGATTATTCACACTAGGCACTGCTTCT 798
QY 108 CCGTCTGAATGGTGTCTGAATACCAATCATGCTCTGCACTGCTTTTCCACTATTTTCA 167
DB 797 CCTCATCTTCAGTTCTTATTTTGGCTTCTGACCCCTTCTTCTTCAACAGCTCTTCT 738
QY 168 CCTCATAATCCAGCTTCTCCAGCAGATTCAGCTCTCTCAGATCCGCCCAACCATCC 227
DB 737 TCATCTTCTCATCATCACTTCCATCTCCATTTGTAATACCTTCTCTCTCTCTCT 678
QY 228 CCATTCAGTCAAAACATTAAAGCCTTCGCAAGGTCACTGCTTCTTCTTCCACCGCGG 287
DB 677 CCATCAGTCTCTCTCTTCAAGTTCCTCTCTCTATCTCTGCTCTCTCTCTCTCTCT 618
QY 288 CCGTGAATGACCAATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 330
DB 617 ACCTGAGCATCTTCAATCATCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 575

RESULT 11
US-10-273-334-26/c
;; Sequence 26, Application US/10273334
;; Publication No. US20030129631A1
;; GENERAL INFORMATION:
;; APPLICANT: Pasternack, Gary R.
;; APPLICANT: Kochnevaev, Gerald J.
;; APPLICANT: Brody, Jonathan R.
;; APPLICANT: Kodkol, Shrihari S.
;; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
;; FILE REFERENCE: 031787.0076
;; CURRENT APPLICATION NUMBER: US/10/273,334
;; CURRENT FILING DATE: 2002-10-18
;; PRIOR APPLICATION NUMBER: US/09/591,500
;; PRIOR FILING DATE: 2000-12-06
;; PRIOR APPLICATION NUMBER: PCT/US98/26433
;; PRIOR FILING DATE: 1998-12-11
;; PRIOR APPLICATION NUMBER: US 60/069,677
;; PRIOR FILING DATE: 1997-12-11
;; NUMBER OF SEQ ID NOS: 51
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 26
;; LENGTH: 905
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (64)..(453)

;; OTHER INFORMATION:
US-10-273-334-26

Query Match 7.1%; Score 43; DB 16; Length 905;
Best Local Similarity 47.0%; Pred. No. 0.013;
Matches 133; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

QY 48 AGAATACTCAAGAAAGGGAATGTAAACATCATGTTTGAATTTGAAATCAACCATG 107
DB 857 ACAGTAAATACAAAAGAAATTTTCAAAATAGATTATTCACACTAGGCACTGCTTCT 798
QY 108 CCGTCTGAATGGTGTCTGAATACCAATCATGCTCTGCACTGCTTTTCCACTATTTTCA 167
DB 797 CCTCATCTTCAGTTCTTATTTTGGCTTCTGACCCCTTCTTCTTCAACAGCTCTTCT 738
QY 168 CCTCATAATCCAGCTTCTCCAGCAGATTCAGCTCTCTCAGATCCGCCCAACCATCC 227
DB 737 TCATCTTCTCATCATCACTTCCATCTCCATTTGTAATACCTTCTCTCTCTCTCT 678
QY 228 CCATTCAGTCAAAACATTAAAGCCTTCGCAAGGTCACTGCTTCTTCTTCCACCGCGG 287
DB 677 CCATCAGTCTCTCTCTTCAAGTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 618
QY 288 CCGTGAATGACCAATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 330
DB 617 ACCTGAGCATCTTCAATCATCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 575

RESULT 12
US-10-273-334-4/c
;; Sequence 4, Application US/10273334
;; Publication No. US20030129631A1
;; GENERAL INFORMATION:
;; APPLICANT: Pasternack, Gary R.
;; APPLICANT: Kochnevaev, Gerald J.
;; APPLICANT: Brody, Jonathan R.
;; APPLICANT: Kodkol, Shrihari S.
;; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
;; FILE REFERENCE: 031787.0076
;; CURRENT APPLICATION NUMBER: US/10/273,334
;; CURRENT FILING DATE: 2002-10-18
;; PRIOR APPLICATION NUMBER: US/09/591,500
;; PRIOR FILING DATE: 2000-12-06
;; PRIOR APPLICATION NUMBER: PCT/US98/26433
;; PRIOR FILING DATE: 1998-12-11
;; PRIOR APPLICATION NUMBER: US 60/069,677
;; PRIOR FILING DATE: 1997-12-11
;; NUMBER OF SEQ ID NOS: 51
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 4
;; LENGTH: 907
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-273-334-4

Query Match 7.1%; Score 43; DB 16; Length 907;
Best Local Similarity 47.0%; Pred. No. 0.013;
Matches 133; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

QY 48 AGAATACTCAAGAAAGGGAATGTAAACATCATGTTTGAATTTGAAATCAACCATG 107
DB 859 ACAGTAAATACAAAAGAAATTTTCAAAATAGATTATTCACACTAGGCACTGCTTCT 800
QY 108 CCGTCTGAATGGTGTCTGAATACCAATCATGCTCTGCACTGCTTTTCCACTATTTTCA 167
DB 799 CCTCATCTTCAGTTCTTATTTTGGCTTCTGACCCCTTCTTCTTCAACAGCTCTTCT 740
QY 168 CCTCATAATCCAGCTTCTCCAGCAGATTCAGCTCTCTCAGATCCGCCCAACCATCC 227
DB 739 TCATCTTCTCATCATCACTTCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 680
QY 228 CCATTCAGTCAAAACATTAAAGCCTTCGCAAGGTCACTGCTTCTTCTTCAACCGCGG 287


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; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: N_region
; LOCATION: (385)..(385)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: N_region
; LOCATION: (409)..(409)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: N_region
; LOCATION: (423)..(423)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: N_region
; LOCATION: (436)..(436)
; OTHER INFORMATION: n = any nucleotide
US-10-260-238-771

```

```

Query Match 6.7%; Score 40.8; DB 12; Length 456;
Best Local Similarity 48.6%; Pred. No. 0.041;
Matches 102; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

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QY 107 GCCGCTGATTGCTGTAATACCAATCATGCTTCGAGTCTTTTCACCTATTTC 166
    |||||
DB 453 GCCGTTGCCGTCGCGCTGCATGCTGATNATTCGCGGCGAGTNGTCGCGGCGGCC 394
    |||||

QY 167 ACCTACATATCCAGTCTTCCGACGATTTCAAGTCTCTACATCCCCCAACCATC 226
    |||||
DB 393 ATGCTTGANCCNGAGCTGACAGCAAGGACCGAGCTNGTCGACGATGATGATCCGTC 334
    |||||

QY 227 CCATTCAGTCAACACTTTAAAGCCTTGCAGGTCACGTCTTCTTCTTCCACCGCC 286
    |||||
DB 333 GCCGTTCTGTGACACGTTGAACGCTCCCGGATCCCTCTCTCTGTCGTCGGGGGC 274
    |||||

QY 287 GCCGTAATGACCAATTCTCTCTCTC 316
    |||||
DB 273 GCCGCCCTTGCCGCCGATGCGCCGCCGCCG 244
    |||||

```

Search completed: January 31, 2004, 02:37:42
Job time : 317 secs

